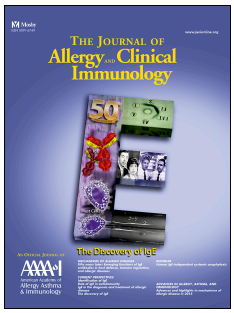
Accepted Manuscript



The Parasitic 68-mer Peptide FhHDM-1 inhibits mixed granulocytic inflammation and airway hyperreactivity in experimental asthma

Akane Tanaka, BSc, Venkata Sita Rama Raju Allam, MS Pharm, Jennifer Simpson, BBiomedSc, Natalia Tiberti, PhD, Jenna Shiels, BSc, Joyce To, BSc, Maria Lund, PhD, Valery Combes, PhD, Sinead Weldon, PhD, Cliff Taggart, PhD, John P. Dalton, PhD, Simon Phipps, PhD, Maria B. Sukkar, PhD, Sheila Donnelly, PhD

PII: S0091-6749(18)30330-0

DOI: 10.1016/j.jaci.2018.01.050

Reference: YMAI 13346

To appear in: *Journal of Allergy and Clinical Immunology*

Received Date: 21 April 2017

Revised Date: 30 December 2017

Accepted Date: 22 January 2018

Please cite this article as: Tanaka A, Allam VSRR, Simpson J, Tiberti N, Shiels J, To J, Lund M, Combes V, Weldon S, Taggart C, Dalton JP, Phipps S, Sukkar MB, Donnelly S, The Parasitic 68-mer Peptide FhHDM-1 inhibits mixed granulocytic inflammation and airway hyperreactivity in experimental asthma, *Journal of Allergy and Clinical Immunology* (2018), doi: 10.1016/j.jaci.2018.01.050.

The Parasitic 68-mer Peptide FhHDM-1 inhibits mixed granulocytic inflammation and airway hyperreactivity in experimental asthma

Clinical Implications:

Peptides secreted by parasitic worms (helminths) have potential in the treatment of asthma and other respiratory conditions in which eosinophilic and/or neutrophilic inflammation plays a pathological role.

Capsule Summary

A peptide derived from the parasitic worm *Fasciola hepatica* inhibits eosinophilic and neutrophilic airway inflammation, mucus production and airway hyperreactivity in a murine model of house dust mite induced asthma.

Key Words:

Helminth, Macrophage, House Dust Mite, Lipopolysaccharide, HMGB1, IL-17, Neutrophils, Eosinophils

Abbreviations:

BALF	Bronchoalveolar lavage fluid
BMDM	Bone marrow derived macrophage
FhHDM-1	*Fasciola hepatica* helminth defense molecule
LPS	Lipopolysaccharide
IPA	Ingenuity Pathway Analysis

Funding:

A Tanaka is supported by an Australian Government Research Training Program Scholarship. VSRR Allam is supported by a University of Technology Sydney Postgraduate Research Scholarship. N Tiberti is supported by the Swiss National Science Foundation (grant n. P300PA_164715). C Taggart and S Weldon are supported by the Medical Research Council. JP Dalton is funded by grants from a European Research Council Advanced Grant (HELIVAC, 322725) and is a member of the Horizon 2020-funded Consortium PARAGONE. S Donnelly is funded by the National Health and Medical Research Council Australia (APP1087341).

Conflicts of Interest: None

Corresponding Author:

A/Prof Sheila Donnelly

School of Life Sciences

University of Technology, Sydney

PO Box 123,

Ultimo 2007, NSW, Australia

Email: Sheila.Donnelly@uts.edu.au

Fax: +61 2 9514 8206

To the Editor,

During infection of their mammalian hosts, parasitic worms (helminths) secrete molecules which modulate the host immune response towards a regulatory phenotype. This ensures the long-term survival of the parasite within its host and also prevents excessive tissue damage mediated by inflammatory immune responses. We reported the identification of a novel immunomodulatory 68-mer peptide secreted by the animal and human parasite *Fasciola hepatica*, termed *F. hepatica* helminth defense molecule 1 (FhHDM-1)[1]. More recently, we showed that FhHDM-1 ameliorates disease in pre-clinical murine models of type 1 diabetes and multiple sclerosis and therefore represents a new bio-active peptide with potential as a novel anti-inflammatory pharmacological therapeutic[2].

The mechanism by which FhHDM-1 protects against immune-related inflammatory disorders is yet to be fully elucidated. In studies thus far, we have shown that FhHDM-1 preferentially binds to macrophages over neutrophils and lymphocytes when administered into the peritoneal cavity of immune competent mice[2]. Additionally, the peptide inhibits pro-inflammatory cytokine release in murine and human macrophages *in vitro*[2, 3]. To pin-point the molecular pathways by which FhHDM-1 exerts its anti-inflammatory effects, we examined global transcriptional changes in murine (Balb/c) bone marrow derived macrophages (BMDMs) treated with a synthetic form of FhHDM-1 for 1 h prior to stimulation with bacterial LPS for either 6 or 24 h. Gene expression was profiled on Agilent microarrays containing probes for 41,346 mouse coding transcripts. This analysis revealed that FhHDM-1 treatment enhanced the expression of 1,363 LPS-regulated genes, and decreased the expression of 1,491 genes by ≥ 2 fold at 6 h. At 24 h, the expression of 988 LPS-regulated genes was increased and 1,292 genes was decreased by ≥ 2 fold (Fig 1A; Online Repository Table 1). Differentially (-2>fold-change>2, P <0.05 with 5% false discovery rate) expressed genes were analysed using Ingenuity Pathway Analysis (IPA) to identify signalling pathways putatively regulated by FhHDM-1 (Fig 1B). Within the top 20 significantly altered

pathways, 16 associated with the activation of pro-inflammatory responses were repressed by FhHDM-1, consistent with its potent anti-inflammatory activity. Notably, IPA analysis predicted that FhHDM-1 inhibits high-mobility group box-1 (HMGB1) signalling and IL-17 mediated allergic inflammation (Fig 1B). The anti-inflammatory effect of the peptide was not specific to Balb/c mice, as BMDMs derived from C57BL6 mice treated with FhHDM-1 showed the same pattern of cytokine suppression in response to LPS (Online Repository Fig E2).

We have previously shown that HMGB1 is an upstream mediator of the allergic asthmatic response in mice[4], and that neutralisation of this protein protects against allergen-induced eosinophilic and neutrophilic inflammation in experimental asthma[4]. IL-17 mediates neutrophilic recruitment to sites of inflammation and is implicated in the neutrophilic asthma phenotype which is relatively resistant to treatment with corticosteroids[5]. Accordingly, we hypothesised that FhHDM-1 has therapeutic potential in allergic asthma, and that it would protect against both eosinophilic and neutrophilic responses.

To test our hypothesis, we employed an experimental mouse model of house-dust mite (HDM) induced allergic asthma, as this model elicits a mixed granulocytic inflammatory response[4]. C57BL6 mice were sensitized to house dust mite extracts (100μg) or saline intranasally, and after 2 weeks, were challenged daily with house dust mite extracts (5 μg) or saline, respectively, for 4 days (See study design, Fig 2A). Mice received an intravenous injection of FhHDM-1 (5, 10 or 25 μg dose) 30 min prior to each house dust mite exposure during the challenge period only. For comparison, mice were also treated with a homologous helminth defense molecule derived from *Schistosoma mansoni* (SmHDM-2) or vehicle control (PBS). FhHDM-1, at both the 10 and 25 μg dose significantly attenuated allergen induced eosinophil, neutrophil and lymphocyte numbers in the BALF (Fig 2B). This effect was specific to FhHDM-1, as neither SmHDM-2 nor PBS had any effect on airway inflammation.

Consistent with this anti-inflammatory effect, FhHDM-1 at both the 10 and 25 μg dose significantly attenuated allergen-induced airway hyper-reactivity (Fig 2C, Online Repository Fig E3). FhHDM-1 also significantly reduced histological evidence of tissue inflammation and mucus production (Fig 2D). Moreover, and consistent with data from the microarray analysis (Online Repository Table 1) and predictions from the IPA analysis (Fig E1B), treatment with FhHDM-1 significantly inhibited allergen-induced expression of macrophage-derived pro-inflammatory mediators, including IL-6, TNF and CCL2, as well as cytokines/chemokines that mediate eosinophil (IL-5, GM-CSF) and neutrophil (CXCL1, GM-CSF) recruitment (Online Repository Table 2). Furthermore, although not statistically significant, FhHDM-1 reduced the expression of IL-4 and IL-17A (Online Repository Table 2).

Other research groups have identified parasite-derived proteins with therapeutic activity in mouse models of asthma. The most well-characterized of these parasite proteins is ES-62, a glycoprotein secreted by the nematode *Acanthocheilonema vitea.* Although effective in suppressing airway inflammation and features of airway remodeling in a mouse model of ovalbumin (OVA) induced asthma, which promotes eosinophilic inflammation, synthetic small molecule analogues of this glycoprotein failed to demonstrate efficacy in clinically relevant models of allergic asthma[6]. Indeed, our data are the first to demonstrate efficacy of a parasite-derived peptide in suppressing neutrophilic inflammation in response to clinically relevant allergens. To validate our finding, we tested the efficacy of FhHDM-1 in a model of LPS-induced neutrophilic inflammation. FhHDM-1 was administered via intraperitoneal injection 24 h and 30 min prior to intratracheal delivery of LPS (1mg/kg). In this model, treatment with FhHDM-1 also resulted in a significant reduction in the number of neutrophils in BALF 6 h after LPS challenge (Online Repository Fig E4).

Asthma is a complex and heterogeneous disease in which multiple molecular pathways are at play. Current therapies based on inhaled corticosteroids are effective in patients in which eosinophilic inflammation is a primary feature, but have limited efficacy in patients with neutrophil-dominant inflammation, or mixed granulocytic inflammation[5]. Recent studies have identified the NLRP3 inflammasome as an important driver of neutrophilic inflammation in asthma[7]. Notably, however, the NLRP3 inflammasome also acts as transcriptional regulator of T-helper 2 cell differentiation[8] which is critical to the development of the eosinophilic inflammation. We have previously shown that FhHDM-1 inhibits lysosomal-associated NLRP3 inflammasome activation in murine and human macrophages *in vitro*[3]. Thus, the protective effects of FhHDM-1 against mixed granulocytic inflammation may be attributed to its capacity to impair the NLRP3 inflammasome[3]. We did not detect increased levels of secreted HMGB1 in BALF at the time point examined in this study (data not shown). However, our transcriptomic studies indicated that FhHDM-1 inhibits HMGB1 signalling. Since HMGB1 is released in response to inflammasome activation in macrophages[9], FhHDM-1 may potentially modulate inflammasome-dependent regulation of HMGB1 signalling in asthma. Certainly, this is an important area for further research. In conclusion, the data support our proposal that the immune modulatory activity of FhHDM-1 is sufficient to prevent granulocytic inflammation and airway hyperreactivity in asthma, and provide a compelling basis for its investigation as a novel therapeutic in this disease.

Akane Tanaka, BSc[a*]

Venkata Sita Rama Raju Allam, MS Pharm[b*]

Jennifer Simpson, BBiomedSc[c]

Natalia Tiberti, PhD[a]

Jenna Shiels, BSc[d, e]

Joyce To, BSc[a]

Maria Lund, PhD[a]

Valery Combes, PhD[a]

Sinead Weldon, PhD[e]

Cliff Taggart, PhD[e]

John P. Dalton, PhD[d]

Simon Phipps, PhD[c]

Maria B. Sukkar, PhD[b*]

Sheila Donnelly, PhD[a*]

From [a]School of Life Sciences, Faculty of Science, The University of Technology Sydney, Ultimo, NSW, Australia; [b]Discipline of Pharmacy, Graduate School of Health, The University of Technology Sydney, Ultimo, NSW, Australia; [c]QIMR Berghofer Medical Research Institute, Herston, QLD, Australia; [d]School of Biological Sciences, Queen's University, Belfast, Northern Ireland; [e]Airway Innate Immunity Group (AiiR), Centre for Experimental Medicine (CEM), School of Medicine, Dentistry and Biomedical Sciences, Queen's University Belfast, Northern Ireland.

* These authors contributed equally

References

1. Robinson MW, Donnelly S, Hutchinson AT, To J, Taylor NL, Norton RS, et al. A Family of Helminth Molecules that Modulate Innate Cell Responses via Molecular Mimicry of Host Antimicrobial Peptides. PLOS Pathogens 2011; 7:e1002042.
2. Lund ME, Greer J, Dixit A, Alvarado R, McCauley-Winter P, To J, et al. A parasite-derived 68-mer peptide ameliorates autoimmune disease in murine models of Type 1 diabetes and multiple sclerosis. Sci Rep 2016; 6:37789.
3. Alvarado R, To J, Lund ME, Pinar A, Mansell A, Robinson MW, et al. The immune modulatory peptide FhHDM-1 secreted by the helminth Fasciola hepatica prevents NLRP3

inflammasome activation by inhibiting endolysosomal acidification in macrophages. FASEB J 2017; 31:85-95.

4. Ullah MA, Loh Z, Gan WJ, Zhang V, Yang H, Li JH, et al. Receptor for advanced glycation end products and its ligand high-mobility group box-1 mediate allergic airway sensitization and airway inflammation. J Allergy Clinical Immunol 2014.
5. Chung KF. Targeting the interleukin pathway in the treatment of asthma. Lancet 2015; 386:1086-96.
6. Janicova L, Rzepecka J, Rodgers DT, Doonan J, Bell KS, Lumb FE, et al. Testing small molecule analogues of the Acanthocheilonema viteae immunomodulator ES-62 against clinically relevant allergens. Parasite Immunol 2016; 38:340-51.
7. Simpson JL, Phipps S, Baines KJ, Oreo KM, Gunawardhana L, Gibson PG. Elevated expression of the NLRP3 inflammasome in neutrophilic asthma. Eur Respir J. 2014; 43:1067-76.
8. Bruchard M, Rebe C, Derangere V, Togbe D, Ryffel B, Boidot R, et al. The receptor NLRP3 is a transcriptional regulator of TH2 differentiation. Nat Immunol 2015; 16:859-70.
9. Lu B, Nakamura T, Inouye K, Li J, Tang Y, Lundback P, et al. Novel role of PKR in inflammasome activation and HMGB1 release. Nature 2012; 488:670-4.

Figure Legends

Figure 1

FhHDM-1 modulates macrophage gene expression. (A) Clustered profiles for all genes expressed in macrophages that were untreated, treated with LPS (10ng/ml) or treated with LPS (10ng/ml) and FhHDM-1 (15μM). Changes in fold expression are depicted for 2 experimental replicates. The color-code key indicates fold increases (red) or decreases (blue) in gene expression. (B) Putative canonical pathways significantly altered by FhHDM-1 in macrophages treated with LPS for 6 h, as determined by IPA® analysis. The color-code key indicates the extent of activation (orange) or inhibition (blue) of a pathway.

Figure 2

FhHDM-1 protects against allergic asthma. (A) Study design. (B) Total and differential cell counts in BALF. (C) Total lung resistance and tissue resistance measured by forced oscillation technique using FlexiVent apparatus. (D) Lung inflammation score and airway mucus score as assessed by hematoxylin and eosin (H&E) and Periodic-Acid Schiff (PAS) staining, respectively. Representative images of H&E (upper panel, x10 original magnification) and PAS (lower panel, x40 original magnification) are shown. Scale bars, 60μm. Data represent mean ± SEM. **P* < .05, ***P* < .01, and ****P* < .001 vs mice treated with PBS. #*P* < .05 and ##*P* < .01 vs mice treated with house dust mite. N = 6 – 8 mice per group.

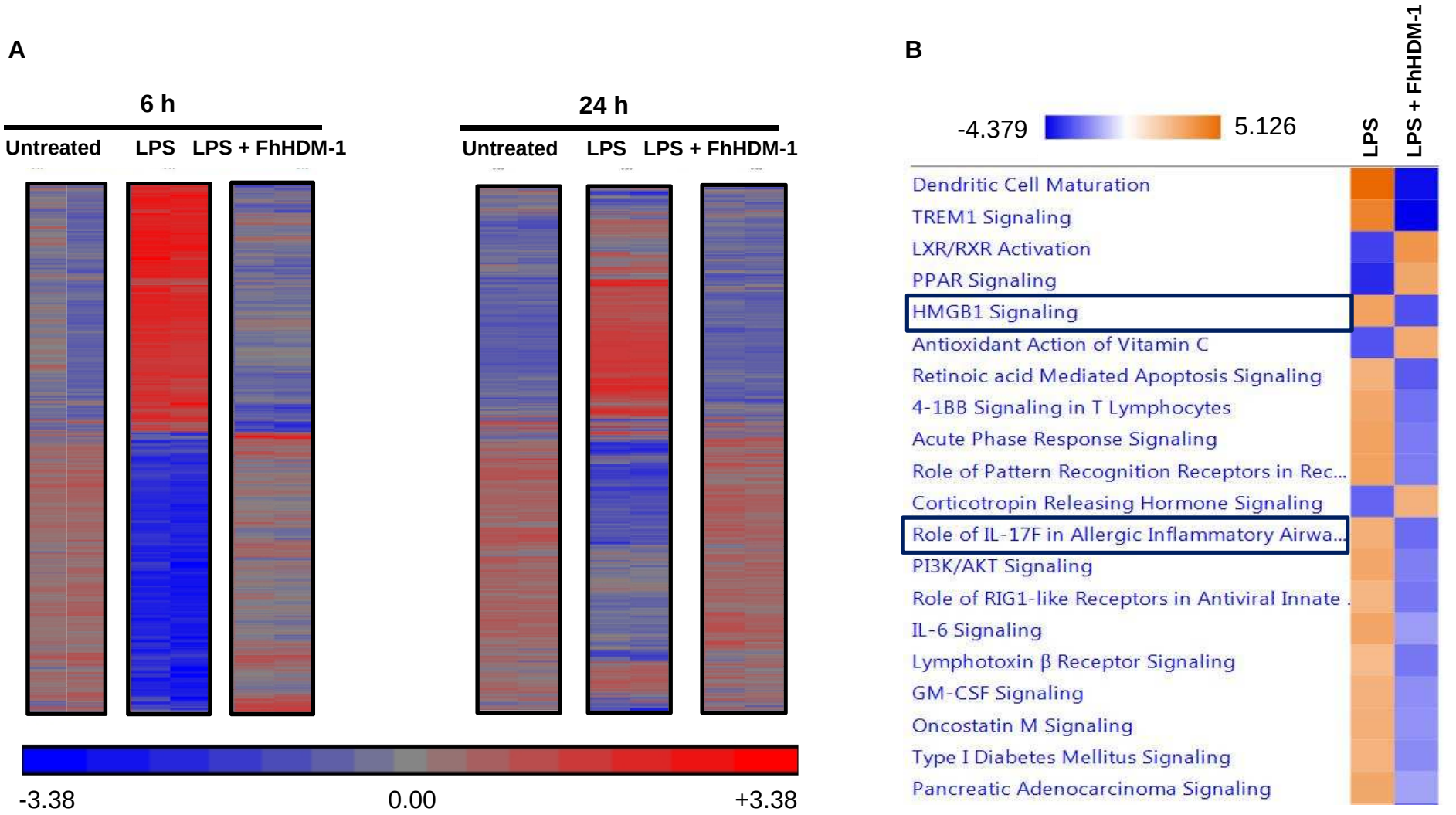
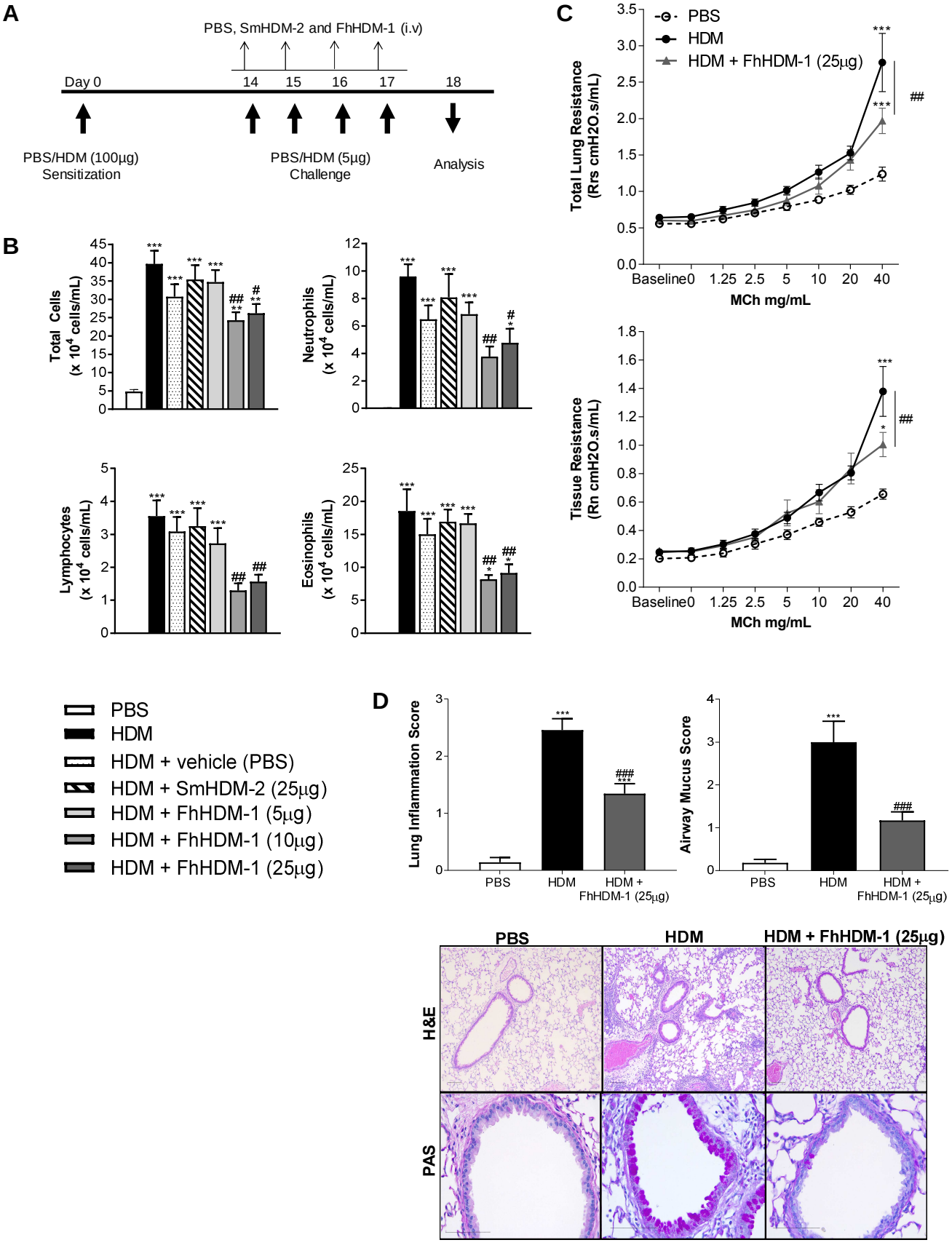

A
6 h
Untreated
LPS
LPS + FhHDM-1
24 h
Untreated
LPS
LPS + FhHDM-1
-3.38
0.00
+3.38
B
-4.379
5.126
LPS
LPS + FhHDM-1
Dendritic Cell Maturation
TREM1 Signaling
LXR/RXR Activation
PPAR Signaling
HMGB1 Signaling
Antioxidant Action of Vitamin C
Retinoic acid Mediated Apoptosis Signaling
4-1BB Signaling in T Lymphocytes
Acute Phase Response Signaling
Role of Pattern Recognition Receptors in Rec...
Corticotropin Releasing Hormone Signaling
Role of IL-17F in Allergic Inflammatory Airwa...
PI3K/AKT Signaling
Role of RIG1-like Receptors in Antiviral Innate ...
IL-6 Signaling
Lymphotoxin β Receptor Signaling
GM-CSF Signaling
Oncostatin M Signaling
Type I Diabetes Mellitus Signaling
Pancreatic Adenocarcinoma Signaling

Figure 1


A
PBS, SmHDM-2 and FhHDM-1 (i.v)
Day 0
14
15
16
17
18
PBS/HDM (100µg)
Sensitization
PBS/HDM (5µg)
Challenge
Analysis
B
Total Cells (x 10^4 cells/mL)
Neutrophils (x 10^4 cells/mL)
Lymphocytes (x 10^4 cells/mL)
Eosinophils (x 10^4 cells/mL)
C
PBS
HDM
HDM + FhHDM-1 (25µg)
Total Lung Resistance (Rrs cmH2O.s/mL)
Tissue Resistance (Rn cmH2O.s/mL)
Baseline0 1.25 2.5 5 10 20 40
MCh mg/mL
PBS
HDM
HDM + vehicle (PBS)
HDM + SmHDM-2 (25µg)
HDM + FhHDM-1 (5µg)
HDM + FhHDM-1 (10µg)
HDM + FhHDM-1 (25µg)
D
Lung Inflammation Score
Airway Mucus Score
PBS
HDM
HDM + FhHDM-1 (25µg)
H&E
PAS

Materials and Methods

Synthesis of parasite peptides

FhHDM-1 and SmHDM-2 were synthesised to 95% purity, with trifluoroacetic acid removed and verified to be endotoxin free (Genscript, USA).

Preparation and stimulation of bone-marrow derived macrophages (BMDMs)

BALB/c and C57BL6 mice were purchased from the Australian Resource Centre (Perth, Australia). All mice were housed under specific pathogen free conditions and procedures were performed at the University of Technology Sydney (UTS), under protocols compliant with the Australian Code for the Care and Use of Animals for Scientific Purposes and approved by the UTS Animal Care and Ethics Committee. Bone marrow cells isolated from BALB/c mice were differentiated for 6 d in RPMI 1640 supplemented with FBS (10%v/v), recombinant M-CSF (50 ng/ml; eBioscience, USA), 2-mercaptoethanol (50µM; Sigma Aldrich) and Penicillin-Streptomycin (100U/ml). BMDMs were confirmed to be $F4/80^+$ $CD11b^+$ by flow cytometry. Cells were resuspended at $1x10^6$ cells/mL and allowed to adhere for 2 h. Cells were then treated with FhHDM-1 (15µM) for 1 h and/or stimulated with LPS (from *E. Coli*, 0111.B4; Sigma Aldrich) at a concentration of 10 ng/ml, for 6 h or 24 h at 37˚C in 5% CO_2.

Gene expression profiling and Ingenuity Pathway Analysis®

After removal of supernatants, cells were homogenised using TRIzol (Life Technologies), as per the manufacturer's protocol. The aqueous phase was then transferred into a genomic DNA eliminating column from the RNeasy Mini Plus kit (Qiagen). RNA was subsequently isolated as per the manufacturer's instructions. Gene expression was assessed using the Affymetrix Mouse Gene 2.1^{ST} Array and performed at the Ramaciotti Centre for Genomics (University of New South Wales, Australia). Analysis of fold changes in gene expression was completed using Partek Genomics Suite (Partek Inc. USA). The generated data files were grouped according to treatment (untreated, LPS or LPS+FhHDM-1), and individual gene lists were generated by one way ANOVA comparison of untreated vs LPS, and LPS vs LPS+FhHDM-1 at 6 h and 24 h time points (-2>fold-change>2, P <0.05 with 5% false discovery rate). Generated gene lists were further analysed using Ingenuity Pathway Analysis (IPA)® software (Ingenuity Systems, Redwood City, CA), where a comparison analysis was conducted. The analysis produced a list of canonical pathways that were assigned an activation z-score, which infers the activation states of predicted transcriptional events as either activated or inhibited.

Quantification of cytokines secreted by macrophages

After 24 h stimulation with LPS, supernatants of C57BL6 BMDMs were harvested and the levels of CCL2, IL-6 and TNF quantified by ELISA (BD Pharmingen, Australia).

Mouse model of allergic asthma

C57BL/6 mice were purchased from the Australian Resource Centre (Perth, Australia). All mice were housed under specific pathogen free conditions and procedures were performed at the University of Technology Sydney (UTS), under protocols compliant with the Australian Code for the Care and Use of Animals for Scientific Purposes and approved by the UTS Animal Care and Ethics Committee. Mice (8 weeks of age) were sensitized to house dust mite allergen (100μg) (Dermatophagoides pteronyssinus, Greer Laboratories, Lenoir, NC, USA) intranasally. After 2 weeks, mice were challenged with house dust mite (5μg) intranasally for 4 days (days 14-17). Control mice were sensitized and challenged with PBS only. Synthetic FhHDM-1 (5, 10, 25μg), SmHDM-1 (25μg) or PBS was administered by intravenous injection through the tail vein 30 min prior to allergen challenge on days 14-17. Mice were exsanguinated with an overdose of pentobarbital (100mg/kg) 24 h after the final allergen challenge on day 18. Study design is shown in Fig 2A.

Analysis of Bronchoalveolar lavage fluid

The lungs were lavaged twice with 0.5mL sterile Hanks Balanced Salt Solution (HBSS). The collected fluid was spun at 3000 rpm for 10 min at 4^{o}C. Cell supernatants were retained for analysis of cytokine/chemokine expression, while cell pellets were resuspended in sterile HBSS for enumeration of total and differential cell counts. To perform differential cell counts, cells were spun on glass slides using a Cytospin 4 Cytocentrifuge (Thermo Fisher Scientific) and were stained with Diff-Quik®. A total of 200 cells were counted to enumerate the differential leukocyte count. Cytokine and chemokine concentrations in BALF were measured using a customized MILLIPLEX® Multiplex Mouse Cytokine/Chemokine assay (Millipore, Billerica, MA) according to manufacturer instructions. The cytokines/chemokines measured were IL-25/IL-17E, IL-22, IL-23, IL-33, eotaxin-1, GM-CSF, IFN-γ, IL-1β, IL-4, IL-5, IL-6, IL-9, IL-12 (p40), IL-12 (p70), IL-13, IL-15, IL-17, KC, MCP-1, MIP-1α, RANTES and TNF. Each sample was analyzed in duplicate using the MAGPIX® System. Five parameter logistic regression was performed to predict the concentration of unknown samples. HMGB1 was measured using a specific ELISA (IBL international) according to manufacturer instructions.

Quantification of airway inflammation

Lung sections were stained with hematoxylin and eosin (H&E) and airway inflammation (inflammatory cell infiltrate) semi-quantified by blind scoring the level of inflammatory cell infiltrates surrounding each airway. Scores ranged from 0-4 (0: no inflammatory cell infiltrates around airway, 1: low level cell infiltrates around part of airway, 2: moderate cell infiltrates around part of or entire airway, 3: significant inflammatory cell infiltrates around part of or entire airway, 4: airway completely surrounded by inflammatory cell infiltrates). Five airways were scored per mouse. All sections were imaged on Aperio Scanscope XT and Leica DM750 Brightfield microscope.

Quantification of mucus

Mucus producing cells were identified by Periodic acid-Schiff (PAS) staining and blind scored from 0 to 5 based on percentage of PAS positive airway epithelial cells (AEC) (0: 0% of total AEC, 1: 1-10% of total AEC, 2: 10-30% of total AEC, 3: 30-50% of total AEC, 4: 50-80% of total AEC, 5: >80% of total AEC). Five airways were scored per mouse.

Airway hyperresponsiveness (AHR)

AHR was measured 24 h after the last allergen challenge by forced oscillation technique using FlexiVent apparatus (SCIREQ, Montreal, Canada). Briefly, mice were anesthetized using a cocktail of xylazine (0.2mg/10gm) and ketamine (0.4mg/10gm body weight). An 18-gauge blunt needle was inserted into the trachea and mice were kept under mechanical ventilation at 200 breaths/min with a delivered tidal volume of 0.25 mL against a positive end-expiratory pressure (PEEP) of 3 cm H_2O. Total lung resistance (Rrs) and tissue resistance (Rn) were recorded by administering increasing doses of nebulized methacholine (0 to 40 mg/mL) (Sigma-Aldrich, St Louis, MO, USA).

Mouse model of LPS induced neutrophilic inflammation

C57BL/6 female mice aged between 10-12 weeks were purchased from Envigo. Housing and experimentation was carried out in accordance with the Animal (Scientific Procedures) Act 1986 and current guidelines approved by the Queen's University Ethical Review Committee. FhHDM-1 (10µg) was administered via intraperitoneal injection 24 h and 30 min prior to intratracheal delivery of *Pseudomonas* LPS (1mg/kg; Sigma-Aldrich, Serotype 10, source strain ATCC 27316). Control mice were treated with PBS only. After 6 h, BALF was collected and total and differential cell counts were performed.

Statistical Analysis

ANOVA for repeated measures was used to determine the levels of difference between groups of mice. Significance levels were set at P = 0.05.

Online Repository Figure Legends

Figure E1.

IPA transcriptional networks of HMGB1 signaling (A) and IL-17 mediated allergic inflammation (B). Signaling components are color coded according to increased (red) or decreased (green) expression in bone-marrow derived macrophages (BMDMs) treated with FhHDM-1 + LPS versus LPS only. The IPA network legend is included in (A).

Figure E2

FhHDM-1 inhibits LPS-induced inflammatory mediator release in BMDMs isolated from C57BL6 mice. Bars represent mean ± SEM from six experiments. ****$P < .0001$ vs untreated cells. #### $P < .0001$ vs cells stimulated with LPS only.

Figure E3

FhHDM-1 inhibits allergen-induced airway hyperreactivity. Total lung resistance and tissue resistance were measured by forced oscillation technique using FlexiVent apparatus. Data represent mean ± SEM. *$P < .05$, and ***$P < .001$ vs mice treated with PBS. ##$P < .01$ vs mice treated with HDM. N = 6 – 8 mice per group.

Figure E4

FhHDM-1 inhibits LPS-induced increases in total cells and neutrophils in mice challenged with an intratracheal delivery of LPS. Bars represent mean ± SEM. *$P < .05$, **$P < .01$, and ***$P < .001$ vs mice treated with HDM or LPS only. N= 6 mice per group.

gene_assignment	Gene Symbol	p-value(6h HDM/LPS vs. 6h LPS)	Fold-Change(6h HDM/LPS vs. 6h LPS)
NM_031168 // Il6 // interleukin 6 // 5 B1|5 15.7 cM // 16193 /// ENSMUST00000026845 //	Il6	0.000352079	-187.713
NM_001167828 // Trim30d // tripartite motif-containing 30D // 7 E3|7 // 209387 /// NM_1	Trim30d	6.06E-05	-172.152
NM_010927 // Nos2 // nitric oxide synthase 2, inducible // 11 B5|11 46.74 cM // 18126 /	Nos2	0.000420919	-145.317
NM_010104 // Edn1 // endothelin 1 // 13 A4|13 20.82 cM // 13614 /// ENSMUST00000021796	Edn1	0.000158878	-90.6905
NM_013730 // Slamf1 // signaling lymphocytic activation molecule family member 1 // 1 H	Slamf1	0.000133758	-80.7479
ENSMUST00000047498 // AA467197 // expressed sequence AA467197 // 2 E5|2 // 433470 /// N	AA467197	5.04E-05	-76.2448
NM_019494 // Cxcl11 // chemokine (C-X-C motif) ligand 11 // 5|5 E3 // 56066 /// NR_0381	Cxcl11	0.00662799	-66.6912
NM_008599 // Cxcl9 // chemokine (C-X-C motif) ligand 9 // 5 E2|5 46.51 cM // 17329 ///	Cxcl9	0.000917271	-60.712
NM_001033415 // Shisa3 // shisa homolog 3 (Xenopus laevis) // 5 C3.1|5 // 330096 /// EN	Shisa3	7.29E-05	-52.7708
XR_378392 // Trim30c // tripartite motif-containing 30C // 7 E3|7 // 434219 /// ENSMUST	Trim30c	3.57E-05	-52.5863
NM_011331 // Ccl12 // chemokine (C-C motif) ligand 12 // 11 C|11 49.9 cM // 20293 /// E	Ccl12	9.65E-05	-50.8604
NM_001142706 // Cfb // complement factor B // 17 B1|17 18.41 cM // 14962 /// NM_008198	Cfb	0.00130591	-50.8015
XM_003945749 // LOC630751 // interferon-inducible GTPase 1-like // --- // 630751 /// XR	LOC630751	8.11E-05	-50.5806
NM_001039647 // Gbp11 // guanylate binding protein 11 // 5 E5|5 // 634650 /// ENSMUST00	Gbp11	0.000167754	-49.824
NM_008352 // Il12b // interleukin 12b // 11 A5-B2|11 25.94 cM // 16160 /// ENSMUST00000	Il12b	4.73E-05	-48.4816
NM_008230 // Hdc // histidine decarboxylase // 2 E5-G|2 61.76 cM // 15186 /// ENSMUST00	Hdc	4.99E-05	-46.5621
NM_009425 // Tnfsf10 // tumor necrosis factor (ligand) superfamily, member 10 // 3 A3|3	Tnfsf10	0.000322518	-42.0204
NM_010554 // Il1a // interleukin 1 alpha // 2 F|2 62.9 cM // 16175 /// XM_006498793 //	Il1a	0.0040839	-40.9628
NM_001256005 // Gbp4 // guanylate binding protein 4 // 5 E5|5 50.68 cM // 17472 /// ENS	Gbp4	0.000245878	-40.7457
NM_011410 // Slfn4 // schlafen 4 // 11 C|11 // 20558 /// ENSMUST00000000208 // Slfn4 //	Slfn4	0.0010104	-38.4837
NM_011407 // Slfn1 // schlafen 1 // 11 C|11 50.3 cM // 20555 /// ENSMUST00000037994 //	Slfn1	0.000520533	-33.5733
NM_172648 // Ifi205 // interferon activated gene 205 // 1 H3|1 80.83 cM // 226695 /// E	Ifi205	0.00349829	-33.4355
ENSMUST00000090406 // BC094916 // cDNA sequence BC094916 // 1 H3|1 // 545384 /// ENSMUS	BC094916	0.000112631	-33.3397
ENSMUST00000128411 // Tgtp2 // T cell specific GTPase 2 // 11 B1.2|11 // 100039796 ///	Tgtp2	0.00103599	-31.8747
NM_011198 // Ptgs2 // prostaglandin-endoperoxide synthase 2 // 1 H1|1 63.84 cM // 19225	Ptgs2	0.000389719	-30.418
NR_029565 // Mir155 // microRNA 155 // 16|16 // 387173 /// ENSMUST00000083463 // Mir155	Mir155	0.00364748	-30.263
NM_009137 // Ccl22 // chemokine (C-C motif) ligand 22 // 8 C5|8 // 20299 /// ENSMUST000	Ccl22	5.79E-05	-29.9854
NM_177371 // Tnfsf15 // tumor necrosis factor (ligand) superfamily, member 15 // 4 C1|4	Tnfsf15	0.000136493	-29.9763
NM_009977 // Cst7 // cystatin F (leukocystatin) // 2|2 G1-G3 // 13011 /// ENSMUST000000	Cst7	9.58E-05	-29.8417
NM_001110517 // Gm14446 // predicted gene 14446 // 19 C1|19 // 667373	Gm14446	2.70E-06	-29.3649
NM_010720 // Lipg // lipase, endothelial // 18|18 E2 // 16891 /// ENSMUST00000066532 //	Lipg	5.85E-05	-28.0617
ENSMUST00000093501 // A530040E14Rik // RIKEN cDNA A530040E14 gene // 1 C5|1 // 621875 /	A530040E14Rik	0.000267293	-25.9454
NR_033483 // U90926 // cDNA sequence U90926 // 5 E2|5 // 57425 /// ENSMUST00000031356 /	U90926	4.41E-06	-24.8312
NM_001033339 // Mmp25 // matrix metallopeptidase 25 // 17 A3.3|17 // 240047 /// ENSMUST	Mmp25	1.27E-05	-24.5774
NM_001146275 // Iigp1 // interferon inducible GTPase 1 // 18 D3|18 // 60440 /// ENSMUST	Iigp1	0.00112326	-23.7751
NM_001083322 // Klrk1 // killer cell lectin-like receptor subfamily K, member 1 // 6 F3	Klrk1	6.91E-05	-23.5335
NM_145636 // Il27 // interleukin 27 // 7 F3|7 // 246779 /// ENSMUST00000058429 // Il27	Il27	0.00182459	-23.3084
XM_006527251 // Ms4a4c // membrane-spanning 4-domains, subfamily A, member 4C // 19 A|1	Ms4a4c	4.57E-05	-22.6564
NM_032541 // Hamp // hepcidin antimicrobial peptide // 7 B1|7 19.27 cM // 84506 /// ENS	Hamp	0.000274544	-21.915
NM_001039646 // Gbp10 // guanylate-binding protein 10 // 5 E5|5 // 626578 /// ENSMUST00	Gbp10	0.000504264	-21.0164
NM_001025606 // Tmem171 // transmembrane protein 171 // 13 D1|13 // 380863 /// ENSMUST0	Tmem171	5.75E-07	-20.5704
NM_009452 // Tnfsf4 // tumor necrosis factor (ligand) superfamily, member 4 // 1 H2.1|1	Tnfsf4	0.000574162	-20.4869
NM_026516 // Tmem178 // transmembrane protein 178 // 17 E3|17 // 68027 /// ENSMUST00000	Tmem178	1.38E-06	-19.5388
NM_001159424 // Il12a // interleukin 12a // 3 E1|3 31.92 cM // 16159 /// NM_008351 // I	Il12a	0.000184269	-17.6491
NM_011246 // Rasgrp1 // RAS guanyl releasing protein 1 // 2 E5|2 59.19 cM // 19419 ///	Rasgrp1	0.00123406	-16.9842
NM_009728 // Atp10a // ATPase, class V, type 10A // 7 C|7 // 11982 /// XM_006540582 //	Atp10a	1.28E-05	-16.6948
NM_172603 // Phf11a // PHD finger protein 11A // 14 C3|14 // 219131 /// ENSMUST00000062	Phf11a	0.000272317	-16.569
NM_008607 // Mmp13 // matrix metallopeptidase 13 // 9|9 A1-A2 // 17386 /// ENSMUST00000	Mmp13	3.24E-05	-16.5414
XR_397994 // BC023105 // cDNA sequence BC023105 // 18 D3|18 // 667597 /// ENSMUST000000	BC023105	1.54E-05	-16.5019
NM_001045543 // Heatr9 // HEAT repeat containing 9 // 11 C|11 // 629303 /// XM_00653390	Heatr9	6.72E-06	-16.3426
NM_144548 // Il23r // interleukin 23 receptor // 6 C1|6 // 209590 /// ENSMUST0000011836	Il23r	3.24E-06	-16.2563
NM_001037925 // BC147527 // cDNA sequence BC147527 // 13|13 // 625360 /// XM_006517732	BC147527	6.81E-06	-16.2362
NM_009801 // Car2 // carbonic anhydrase 2 // 3 A1|3 3.23 cM // 12349 /// XM_006530050 /	Car2	4.11E-05	-16.1024
---		6.91E-05	-16.0864
NM_013654 // Ccl7 // chemokine (C-C motif) ligand 7 // 11 C|11 49.83 cM // 20306 /// EN	Ccl7	4.21E-07	-15.3987
NM_001045526 // Scimp // SLP adaptor and CSK interacting membrane protein // 11 B3|11 /	Scimp	4.65E-06	-15.2661
ENSMUST00000103463 // Ighv14-1 // immunoglobulin heavy variable 14-1 // --- // --- ///	Ighv14-1	0.000113295	-15.1501
NM_013652 // Ccl4 // chemokine (C-C motif) ligand 4 // 11 C|11 51.09 cM // 20303 /// EN	Ccl4	0.000206747	-14.7649
NM_007646 // Cd38 // CD38 antigen // 5 B3|5 23.85 cM // 12494 /// ENSMUST00000030964 //	Cd38	0.00198458	-14.6528
NM_009890 // Ch25h // cholesterol 25-hydroxylase // 19 C1|19 // 12642 /// ENSMUST000000	Ch25h	2.50E-06	-14.3695
NM_177290 // Itgb8 // integrin beta 8 // 12 F2|12 // 320910 /// XM_006516016 // Itgb8 /	Itgb8	0.00113658	-14.3692
NM_011333 // Ccl2 // chemokine (C-C motif) ligand 2 // 11 C-E1|11 49.82 cM // 20296 ///	Ccl2	6.36E-06	-14.3116
NM_199016 // Enpp4 // ectonucleotide pyrophosphatase/phosphodiesterase 4 // 17 B3|17 //	Enpp4	4.27E-06	-14.124
NM_001205053 // Jdp2 // Jun dimerization protein 2 // 12|12 D3 // 81703 /// NM_030887 /	Jdp2	3.66E-06	-13.8975
NM_011693 // Vcam1 // vascular cell adhesion molecule 1 // 3 G1|3 50.17 cM // 22329 ///	Vcam1	0.000608247	-13.693
NM_001271498 // Il15ra // interleukin 15 receptor, alpha chain // 2 A1|2 8.97 cM // 161	Il15ra	5.84E-06	-13.5586
NM_175026 // Pyhin1 // pyrin and HIN domain family, member 1 // 1 H3|1 // 236312 /// EN	Pyhin1	0.000601279	-13.4304
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	8.25E-07	-13.3772
NM_175449 // Fam26f // family with sequence similarity 26, member F // 10 B1|10 // 2159	Fam26f	0.000197491	-13.3066
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	2.69E-06	-13.251
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	2.69E-06	-13.251
NM_001013832 // Gpr31b // G protein-coupled receptor 31, D17Leh66b region // 17 A1|17 8	Gpr31b	7.55E-05	-13.0761
ENSMUST00000103475 // Ighv14-4 // immunoglobulin heavy variable 14-4 // --- // --- ///	Ighv14-4	3.67E-05	-12.8769
NM_001168660 // Apol9b // apolipoprotein L 9b // 15 E1|15 // 71898 /// NM_173743 // Apo	Apol9b	6.02E-05	-12.6713
NM_001038643 // Slco3a1 // solute carrier organic anion transporter family, member 3a1	Slco3a1	1.68E-05	-12.5854
NM_010846 // Mx1 // myxovirus (influenza virus) resistance 1 // 16 C4|16 57.46 cM // 17	Mx1	0.00229257	-12.4639
NM_001101475 // F830016B08Rik // RIKEN cDNA F830016B08 gene // 18 D3|18 // 240328 /// X	F830016B08Rik	0.000335906	-12.4454
NM_145209 // Oasl1 // 2-5 oligoadenylate synthetase-like 1 // 5 F|5 // 231655 /// ENSMU	Oasl1	0.000738364	-12.43
NM_172777 // Gbp9 // guanylate-binding protein 9 // 5 E5|5 // 236573 /// XM_006534923 /	Gbp9	6.84E-05	-12.3814
ENSMUST00000057784 // Slc7a2 // solute carrier family 7 (cationic amino acid transporte	Slc7a2	0.000307879	-11.9595
NM_001242368 // F10 // coagulation factor X // 8 A1.1|8 5.73 cM // 14058 /// NM_007972	F10	1.01E-05	-11.9344
NM_001033767 // Gm4951 // predicted gene 4951 // 18 D3|18 // 240327 /// ENSMUST00000031	Gm4951	0.0013424	-11.8381
NM_001201367 // Tmem200b // transmembrane protein 200B // 4 D2.3|4 // 623230 /// ENSMUS	Tmem200b	1.30E-07	-11.6745
NM_001085502 // Nt5c1a // 5-nucleotidase, cytosolic IA // 4 D2.2|4 // 230718 /// XR_376	Nt5c1a	1.31E-05	-11.5855
NM_001276248 // Cp // ceruloplasmin // 3|3 D // 12870 /// NM_001276250 // Cp // cerulop	Cp	8.92E-06	-11.533
ENSMUST00000127563 // Gm13822 // predicted gene 13822 // --- // ---	Gm13822	0.000262329	-11.4441
NM_008491 // Lcn2 // lipocalin 2 // 2 A3|2 22.09 cM // 16819 /// ENSMUST00000050785 //	Lcn2	0.000189505	-11.351
NM_010612 // Kdr // kinase insert domain protein receptor // 5 C3.3|5 40.23 cM // 16542	Kdr	8.36E-06	-11.1438

NM_001034859 // Gm4841 // predicted gene 4841 // 18 D3|18 // 225594 /// ENSMUST00000090	Gm4841	0.000594742	-11.0274
NM_010479 // Hspa1a // heat shock protein 1A // 17 B1|17 18.51 cM // 193740 /// ENSMUST	Hspa1a	9.56E-06	-10.806
---		8.72E-06	-10.8042
NM_001162883 // Apol9a // apolipoprotein L 9a // 15 E1|15 // 223672 /// NM_173786 // Ap	Apol9a	5.66E-07	-10.6271
NM_009630 // Adora2a // adenosine A2a receptor // 10 B5.3|10 // 11540 /// XM_006513094	Adora2a	0.000866737	-10.4452
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	1.15E-05	-10.4312
NM_013606 // Mx2 // myxovirus (influenza virus) resistance 2 // 16 C4|16 57.51 cM // 17	Mx2	0.00078845	-10.3857
ENSMUST00000173680 // Gm20481 // predicted gene 20481 // --- // --- /// BC054065 // Hsp	Gm20481	6.49E-07	-10.2733
NM_199015 // Phf11d // PHD finger protein 11D // 14 C3|14 31.48 cM // 219132 /// XM_006	Phf11d	3.15E-05	-10.1232
NM_001289492 // Gbp3 // guanylate binding protein 3 // 3 H1|3 // 55932 /// NM_001289493	Gbp3	0.00656795	-10.0607
ENSMUST00000134150 // Batf2 // basic leucine zipper transcription factor, ATF-like 2 //	Batf2	6.39E-06	-9.95176
NM_009742 // Bcl2a1a // B cell leukemia/lymphoma 2 related protein A1a // 9 E3.1|9 47.2	Bcl2a1a	0.000122452	-9.80143
NM_001033335 // Serpina3f // serine (or cysteine) peptidase inhibitor, clade A, member	Serpina3f	0.000138876	-9.72061
NM_001164329 // Gm6904 // predicted gene 6904 // 14 C3|14 // 628693 /// ENSMUST00000168	Gm6904	4.58E-06	-9.5647
NM_001025246 // Trp53i11 // transformation related protein 53 inducible protein 11 // 2	Trp53i11	1.10E-05	-9.26376
NM_029639 // Plet1 // placenta expressed transcript 1 // 9|9 B // 76509 /// ENSMUST0000	Plet1	2.37E-06	-9.19854
NM_010548 // Il10 // interleukin 10 // 1 E4|1 56.89 cM // 16153 /// ENSMUST00000016673	Il10	2.85E-06	-9.1824
ENSMUST00000178021 // Ifitm7 // interferon induced transmembrane protein 7 // 16 A1|16	Ifitm7	6.73E-05	-9.0119
XM_006498216 // Ptges // prostaglandin E synthase // 2 B|2 21.75 cM // 64292 /// NM_022	Ptges	0.000678447	-8.93959
NM_010090 // Dusp2 // dual specificity phosphatase 2 // 2 F1|2 // 13537 /// ENSMUST0000	Dusp2	0.00104714	-8.91961
NM_008360 // Il18 // interleukin 18 // 9 A5.3|9 27.75 cM // 16173 /// XM_006510023 // I	Il18	1.96E-06	-8.90737
NM_029612 // Slamf9 // SLAM family member 9 // 1 H3|1 // 98365 /// XM_006497067 // Slam	Slamf9	1.87E-05	-8.89449
NM_007535 // Bcl2a1c // B cell leukemia/lymphoma 2 related protein A1c // 9 F3|9 // 120	Bcl2a1c	0.000205658	-8.89343
NM_001171007 // Nod1 // nucleotide-binding oligomerization domain containing 1 // 6 B3|	Nod1	1.76E-06	-8.74022
NM_001177349 // Pydc4 // pyrin domain containing 4 // 1 H3|1 // 623121 /// NM_001177350	Pydc4	4.05E-05	-8.67494
NM_001164289 // Phf11c // PHD finger protein 11C // 14 C3|14 // 628705 /// ENSMUST00000	Phf11c	4.26E-05	-8.55533
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// ENSMUST0000	Gm7609	0.000440049	-8.5357
NM_011909 // Usp18 // ubiquitin specific peptidase 18 // 6 F|6 57.17 cM // 24110 /// EN	Usp18	0.000196903	-8.39555
XR_400650 // LOC102634900 // uncharacterized LOC102634900 // --- // 102634900 /// ENSMU	LOC102634900	4.41E-07	-8.38139
---		0.00158088	-8.35675
NM_001291220 // Isg20 // interferon-stimulated protein // 7 D3|7 // 57444 /// NM_001113	Isg20	0.000253043	-8.32183
---		0.00580692	-8.3183
NM_172796 // Slfn9 // schlafen 9 // 11 C|11 // 237886 /// ENSMUST00000038211 // Slfn9 /	Slfn9	9.15E-05	-8.16161
ENSMUST00000162784 // Gm16094 // predicted gene 16094 // --- // ---	Gm16094	3.09E-05	-8.08667
NM_001080813 // Rab11fip1 // RAB11 family interacting protein 1 (class I) // 8|8 A3 //	Rab11fip1	9.29E-05	-8.04753
ENSMUST00000137792 // Rsad2 // radical S-adenosyl methionine domain containing 2 // 12|	Rsad2	0.00629878	-8.03369
NM_009421 // Traf1 // TNF receptor-associated factor 1 // 2 B|2 // 22029 /// XM_0064978	Traf1	0.00221431	-8.0319
---		0.000914691	-8.02224
NM_008867 // Pla2r1 // phospholipase A2 receptor 1 // 2 C1.1|2 // 18779 /// ENSMUST0000	Pla2r1	0.000355214	-7.9467
NM_008204 // H2-M2 // histocompatibility 2, M region locus 2 // 17 B1|17 19.16 cM // 14	H2-M2	0.000420205	-7.94478
---		0.000770731	-7.89625
NR_035466 // Mir1945 // microRNA 1945 // 16|16 6.4 cM // 100316833 /// ENSMUST000001579	Mir1945	0.000356706	-7.85203
NM_153511 // Il1f9 // interleukin 1 family, member 9 // 2 A3|2 16.24 cM // 215257 /// E	Il1f9	2.04E-05	-7.6936
NM_001145827 // Stk40 // serine/threonine kinase 40 // 4 D2.2|4 // 74178 /// NM_028800	Stk40	5.49E-07	-7.6542
NR_110420 // Ptgs2os2 // prostaglandin-endoperoxide synthase 2, opposite strand 2 // 1	Ptgs2os2	0.000566164	-7.59696
NM_010276 // Gem // GTP binding protein (gene overexpressed in skeletal muscle) // 4 A1	Gem	5.39E-05	-7.56326
NM_001033207 // Nlrc5 // NLR family, CARD domain containing 5 // 8 C5|8 // 434341 /// X	Nlrc5	5.64E-05	-7.544
NM_008013 // Fgl2 // fibrinogen-like protein 2 // 5 A3|5 9.83 cM // 14190 /// ENSMUST00	Fgl2	7.80E-05	-7.5175
NM_008479 // Lag3 // lymphocyte-activation gene 3 // 6 F2|6 // 16768 /// ENSMUST0000003	Lag3	3.42E-06	-7.50915
NM_001037917 // Gm6377 // predicted gene 6377 // X D|X // 622976 /// ENSMUST00000060013	Gm6377	1.48E-05	-7.50625
---		0.000927018	-7.48742
NM_017370 // Hp // haptoglobin // 8 D3|8 57.11 cM // 15439 /// ENSMUST00000074898 // Hp	Hp	1.75E-05	-7.46036
ENSMUST00000023341 // Cd200 // CD200 antigen // 16 A1|16 29.53 cM // 17470 /// ENSMUST0	Cd200	7.43E-06	-7.44665
NM_029472 // Gstt4 // glutathione S-transferase, theta 4 // 10 C1|10 // 75886 /// ENSMU	Gstt4	1.86E-05	-7.41363
NM_019450 // Il1f6 // interleukin 1 family, member 6 // 2 A3|2 16.26 cM // 54448 /// EN	Il1f6	1.03E-07	-7.39034
NR_040453 // Gm17757 // GTPase, very large interferon inducible 1 pseudogene // 7|7 //	Gm17757	0.000125395	-7.33109
NM_178890 // Abtb2 // ankyrin repeat and BTB (POZ) domain containing 2 // 2 E2|2 // 993	Abtb2	3.72E-08	-7.31221
NM_016767 // Batf // basic leucine zipper transcription factor, ATF-like // 12 D2|12 //	Batf	3.06E-06	-7.27959
NM_001164059 // Sell // selectin, lymphocyte // 1 H2.2|1 71.37 cM // 20343 /// NM_01134	Sell	9.13E-07	-7.25382
---		0.000213685	-7.22871
NM_001271603 // Socs1 // suppressor of cytokine signaling 1 // 16 A1|16 5.81 cM // 1270	Socs1	0.000308991	-7.16716
NM_001271416 // Ly6a // lymphocyte antigen 6 complex, locus A // 15 D3|15 34.29 cM // 1	Ly6a	7.49E-08	-7.15985
NM_010478 // Hspa1b // heat shock protein 1B // 17 B1|17 18.5 cM // 15511 /// ENSMUST00	Hspa1b	0.000153332	-7.14649
NM_021443 // Ccl8 // chemokine (C-C motif) ligand 8 // 11 C|11 49.91 cM // 20307 /// EN	Ccl8	4.14E-05	-7.12765
XM_001473524 // Gm2427 // predicted gene 2427 // 1 C5|1 // 100039794	Gm2427	0.00238192	-7.10566
NM_030701 // Hcar2 // hydroxycarboxylic acid receptor 2 // 5 F|5 // 80885 /// ENSMUST00	Hcar2	0.00329191	-7.04514
NM_133664 // Lad1 // ladinin // 1 E4|1 // 16763 /// ENSMUST00000038760 // Lad1 // ladin	Lad1	8.36E-07	-7.02736
XM_006502252 // Rapgef2 // Rap guanine nucleotide exchange factor (GEF) 2 // 3 E3|3 //	Rapgef2	2.65E-05	-7.02572
ENSMUST00000180551 // Gm26584 // predicted gene, 26584 // --- // ---	Gm26584	0.000136766	-7.00216
NM_001002268 // Gpr126 // G protein-coupled receptor 126 // 10 A2|10 // 215798 /// ENSM	Gpr126	2.21E-05	-6.99669
NM_001039701 // Il1rn // interleukin 1 receptor antagonist // 2 A3|2 16.36 cM // 16181	Il1rn	2.04E-05	-6.96281
NM_001164327 // Phf11b // PHD finger protein 11B // 14 C3|14 // 236451 /// ENSMUST00000	Phf11b	0.000450708	-6.89147
NM_178759 // Timd4 // T cell immunoglobulin and mucin domain containing 4 // 11 B1.1|11	Timd4	0.000460409	-6.88102
NR_040453 // Gm17757 // GTPase, very large interferon inducible 1 pseudogene // 7|7 //	Gm17757	0.00015864	-6.84672
ENSMUST00000110200 // Sntb1 // syntrophin, basic 1 // 15 D1|15 22.14 cM // 20649 /// BC	Sntb1	4.40E-10	-6.79585
---		0.00403516	-6.78129
ENSMUST00000103468 // Igh-V11 // immunoglobulin heavy chain (V11 family) // 12 F1|12 //	Igh-V11	8.54E-05	-6.77336
---		0.000211601	-6.76834
NM_183162 // Helz2 // helicase with zinc finger 2, transcriptional coactivator // 2 H4|	Helz2	0.000202825	-6.73343
NM_153287 // Csrnp1 // cysteine-serine-rich nuclear protein 1 // 9 F4|9 // 215418 /// X	Csrnp1	2.15E-08	-6.70599
NM_001083312 // Gbp7 // guanylate binding protein 7 // 3 H1|3 // 229900 /// NM_145545 /	Gbp7	0.0045267	-6.70578
NM_015811 // Rgs1 // regulator of G-protein signaling 1 // 1 F|1 62.56 cM // 50778 ///	Rgs1	2.79E-07	-6.70249
NM_008367 // Il2ra // interleukin 2 receptor, alpha chain // 2 A2-A3|2 8.91 cM // 16184	Il2ra	5.67E-05	-6.5894
ENSMUST00000070435 // Fabp3-ps1 // fatty acid binding protein 3, muscle and heart, pseu	Fabp3-ps1	1.39E-05	-6.55506
NM_029495 // Epsti1 // epithelial stromal interaction 1 (breast) // 14 D3|14 // 108670	Epsti1	0.000107394	-6.52711
NM_001254747 // Il15 // interleukin 15 // 8 C2|8 39.33 cM // 16168 /// NM_008357 // Il1	Il15	3.51E-05	-6.46136
NM_001177471 // Gm15056 // predicted gene 15056 // 8 A2|8 // 100504014 /// ENSMUST00000	Gm15056	0.000258381	-6.45464
---		0.00210122	-6.41436
---		0.000445895	-6.40836

NM_001081249 // Vcan // versican // 13 C3|13 45.5 cM // 13003 /// NM_001134474 // Vcan	Vcan	4.10E-07	-6.39956
NM_001008497 // P2ry14 // purinergic receptor P2Y, G-protein coupled, 14 // 3 D|3 28.96	P2ry14	4.77E-08	-6.38648
NM_001290646 // Lhx2 // LIM homeobox protein 2 // 2 B|2 // 16870 /// NM_010710 // Lhx2	Lhx2	0.000142503	-6.35913
NR_027919 // Bambi-ps1 // BMP and activin membrane-bound inhibitor, pseudogene (Xenopus	Bambi-ps1	6.30E-05	-6.31234
NM_026840 // Pdgfrl // platelet-derived growth factor receptor-like // 8 A4|8 // 68797	Pdgfrl	1.94E-07	-6.30366
NM_001252600 // Irf7 // interferon regulatory factor 7 // 7 F5|7 // 54123 /// NM_001252	Irf7	0.000265784	-6.24885
ENSMUST00000120997 // Rnd1 // Rho family GTPase 1 // 15 F1|15 // 223881 /// BC048531 //	Rnd1	1.79E-05	-6.22523
NM_001286062 // Angpt1 // angiopoietin 1 // 15 B3.1|15 16.69 cM // 11600 /// NM_009640	Angpt1	6.73E-06	-6.20891
NM_001177752 // Pfkfb3 // 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 // 2 A1	Pfkfb3	3.10E-06	-6.19588
NM_001033780 // I830077J02Rik // RIKEN cDNA I830077J02 gene // 3 F2.2|3 // 433638 /// X	I830077J02Rik	8.61E-09	-6.18071
NM_001163440 // Mov10 // Moloney leukemia virus 10 // 3|3 F2 // 17454 /// NM_001163441	Mov10	3.37E-06	-6.09729
NM_008332 // Ifit2 // interferon-induced protein with tetratricopeptide repeats 2 // 19	Ifit2	0.00613412	-6.08241
NR_003507 // Oas1b // 2-5 oligoadenylate synthetase 1B // 5 F|5 60.64 cM // 23961 /// E	Oas1b	3.95E-05	-6.0571
NM_133501 // Ntng2 // netrin G2 // 2 B|2 19.57 cM // 171171 /// ENSMUST00000048455 // N	Ntng2	1.79E-06	-6.05336
ENSMUST00000060442 // Gpr85 // G protein-coupled receptor 85 // 6 A1|6 // 64450 /// NM_	Gpr85	0.000218572	-6.05227
NM_001081187 // Htra4 // HtrA serine peptidase 4 // 8 A2|8 // 330723 /// ENSMUST0000008	Htra4	4.22E-05	-6.0049
---		0.00256689	-5.97279
XM_006535862 // LOC100041708 // nuclear body protein SP140-like // 1|1 // 100041708	LOC100041708	0.00030833	-5.95034
NM_201368 // Xkr8 // X Kell blood group precursor related family member 8 homolog // 4	Xkr8	7.02E-07	-5.94836
ENSMUST00000082757 // Gm24149 // predicted gene, 24149 // --- // ---	Gm24149	0.000469826	-5.88602
NM_138648 // Olr1 // oxidized low density lipoprotein (lectin-like) receptor 1 // 6 F3|	Olr1	0.000905739	-5.86485
NM_001172205 // Arid5a // AT rich interactive domain 5A (MRF1-like) // 1 B|1 // 214855	Arid5a	1.10E-06	-5.86051
---		0.00478412	-5.85967
NM_018738 // Igtp // interferon gamma induced GTPase // 11 B1.3|11 36.01 cM // 16145 //	Igtp	0.000687588	-5.85232
NM_172621 // Clic5 // chloride intracellular channel 5 // 17|17 C // 224796 /// XM_0065	Clic5	0.000133461	-5.85195
NM_001243039 // Gm4070 // predicted gene 4070 // 7 E3|7 // 100042856 /// NM_029000 // G	Gm4070	2.24E-05	-5.84478
NM_001161798 // Mthfr // 5,10-methylenetetrahydrofolate reductase // 4 E2|4 78.67 cM //	Mthfr	2.13E-07	-5.83239
NM_027450 // Glipr2 // GLI pathogenesis-related 2 // 4 B1|4 // 384009 /// ENSMUST000000	Glipr2	2.34E-06	-5.78801
ENSMUST00000068569 // Bcl2a1b // B cell leukemia/lymphoma 2 related protein A1b // 9 E3	Bcl2a1b	4.25E-06	-5.77873
NM_010751 // Mxd1 // MAX dimerization protein 1 // 6 D1|6 37.75 cM // 17119 /// ENSMUST	Mxd1	5.53E-06	-5.77106
---		0.000327208	-5.75527
NM_007536 // Bcl2a1d // B cell leukemia/lymphoma 2 related protein A1d // 9 E3.1|9 // 1	Bcl2a1d	2.80E-05	-5.64471
NM_126166 // Tlr3 // toll-like receptor 3 // 8|8 B2 // 142980 /// XM_006509278 // Tlr3	Tlr3	5.59E-06	-5.63035
NM_009404 // Tnfsf9 // tumor necrosis factor (ligand) superfamily, member 9 // 17 D|17	Tnfsf9	0.0054702	-5.61702
NM_001199733 // Daxx // Fas death domain-associated protein // 17 B1|17 17.98 cM // 131	Daxx	4.12E-05	-5.60431
ENSMUST00000156081 // Gm12840 // predicted gene 12840 // --- // ---	Gm12840	0.00052171	-5.60417
NM_021394 // Zbp1 // Z-DNA binding protein 1 // 2 H3|2 // 58203 /// ENSMUST00000029018	Zbp1	0.000350719	-5.57807
NM_001243039 // Gm4070 // predicted gene 4070 // 7 E3|7 // 100042856 /// NM_029000 // G	Gm4070	0.000183133	-5.5615
NM_029005 // Mlkl // mixed lineage kinase domain-like // 8|8 D3 // 74568 /// XM_0065314	Mlkl	2.90E-05	-5.55206
ENSMUST00000112574 // Klf8 // Kruppel-like factor 8 // X F3|X // 245671 /// NM_173780 /	Klf8	9.89E-05	-5.54461
NM_001081427 // Flnb // filamin, beta // 14 A1|14 // 286940 /// NM_134080 // Flnb // fi	Flnb	7.07E-06	-5.53354
NM_001164566 // Spats2l // spermatogenesis associated, serine-rich 2-like // 1|1 C2 //	Spats2l	0.000480249	-5.52726
---		0.00271712	-5.51996
NM_007707 // Socs3 // suppressor of cytokine signaling 3 // 11 E2|11 // 12702 /// ENSMU	Socs3	0.00213594	-5.49358
NM_025658 // Ms4a4d // membrane-spanning 4-domains, subfamily A, member 4D // 19 A|19 /	Ms4a4d	0.000109083	-5.46808
NM_001252374 // Nt5c3 // 5-nucleotidase, cytosolic III // 6 B3|6 // 107569 /// XM_00650	Nt5c3	6.90E-05	-5.4597
NM_001004762 // Pla2g4c // phospholipase A2, group IVC (cytosolic, calcium-independent)	Pla2g4c	0.00016746	-5.43261
NM_001141948 // Nmi // N-myc (and STAT) interactor // 2|2 C1 // 64685 /// NM_001141949	Nmi	3.03E-06	-5.38282
ENSMUST00000145961 // Gm12764 // predicted gene 12764 // --- // ---	Gm12764	4.38E-06	-5.37002
NM_007719 // Ccr7 // chemokine (C-C motif) receptor 7 // 11 D|11 // 12775 /// XM_006532	Ccr7	0.000955136	-5.33796
NM_145226 // Oas3 // 2-5 oligoadenylate synthetase 3 // 5 F|5 60.64 cM // 246727 /// EN	Oas3	0.000114475	-5.30533
NM_029809 // 2310014L17Rik // RIKEN cDNA 2310014L17 gene // 7 A1|7 // 381845 /// ENSMUS	2310014L17Rik	0.00036202	-5.29897
NM_146786 // Olfr914 // olfactory receptor 914 // 9 A5|9 // 258782 /// ENSMUST000000577	Olfr914	7.49E-05	-5.29817
NM_007981 // Acsl1 // acyl-CoA synthetase long-chain family member 1 // 8|8 B2 // 14081	Acsl1	0.00060057	-5.29736
NM_007611 // Casp7 // caspase 7 // 19 D2|19 51.84 cM // 12369 /// ENSMUST00000026062 //	Casp7	1.39E-05	-5.29503
NM_001159402 // Upp1 // uridine phosphorylase 1 // 11|11 A1-2 // 22271 /// XM_006514667	Upp1	0.00128968	-5.29337
ENSMUST00000161540 // Gm17017 // predicted gene 17017 // --- // ---	Gm17017	4.76E-07	-5.25234
NM_019440 // Irgm2 // immunity-related GTPase family M member 2 // 11 B1.3|11 // 54396	Irgm2	0.000170735	-5.25119
NM_001164477 // Ifih1 // interferon induced with helicase C domain 1 // 2|2 C3 // 71586	Ifih1	0.000472853	-5.22645
NR_037278 // Mir3095 // microRNA 3095 // 4|4 32.2 cM // 100526502 /// ENSMUST0000017555	Mir3095	1.44E-05	-5.22033
NM_008869 // Pla2g4a // phospholipase A2, group IVA (cytosolic, calcium-dependent) // 1	Pla2g4a	1.35E-05	-5.20299
NR_029527 // Mirlet7i // microRNA let7i // 10|10 // 387251 /// ENSMUST00000083472 // Mi	Mirlet7i	0.00021497	-5.18986
NM_021893 // Cd274 // CD274 antigen // 19|19 C2 // 60533 /// ENSMUST00000016640 // Cd27	Cd274	5.44E-05	-5.16336
NM_013632 // Pnp // purine-nucleoside phosphorylase // 14 B-C1|14 26.31 cM // 18950 ///	Pnp	5.01E-06	-5.15841
NR_028589 // Gm14005 // predicted gene 14005 // 2 F1|2 // 100043424 /// NR_028590 // Gm	Gm14005	3.66E-05	-5.15076
---		0.000446993	-5.1483
ENSMUST00000181444 // Gm26589 // predicted gene, 26589 // --- // --- /// XR_379475 // L	Gm26589	2.66E-06	-5.12128
ENSMUST00000111253 // Setdb2 // SET domain, bifurcated 2 // 14 C3|14 // 239122 /// AK08	Setdb2	5.25E-06	-5.12089
NM_001177576 // Slc25a22 // solute carrier family 25 (mitochondrial carrier, glutamate)	Slc25a22	1.59E-07	-5.10755
ENSMUST00000181565 // Gm26522 // predicted gene, 26522 // --- // ---	Gm26522	0.000691473	-5.08544
NM_027081 // Dennd6b // DENN/MADD domain containing 6B // 15 E3|15 // 69440 /// ENSMUST	Dennd6b	2.75E-05	-5.07813
NM_001293783 // Ddx60 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 // 8 B3.1|8 // 23431	Ddx60	0.000297328	-5.05199
NM_011562 // Tdgf1 // teratocarcinoma-derived growth factor 1 // 9 F3|9 60.79 cM // 216	Tdgf1	0.000235678	-5.03946
NM_139269 // Pla2g16 // phospholipase A2, group XVI // 19 A|19 // 225845 /// XM_0065269	Pla2g16	0.000101568	-5.0065
NM_172488 // Lacc1 // laccase (multicopper oxidoreductase) domain containing 1 // 14 D3	Lacc1	7.78E-05	-4.98429
NM_025992 // Herc6 // hect domain and RLD 6 // 6 C1|6 // 67138 /// ENSMUST00000031817 /	Herc6	0.000141657	-4.96207
NM_001082552 // Trim21 // tripartite motif-containing 21 // 7 F1|7 // 20821 /// NM_0092	Trim21	5.02E-05	-4.95933
NM_008380 // Inhba // inhibin beta-A // 13 A1|13 5.85 cM // 16323 /// ENSMUST0000004260	Inhba	1.21E-05	-4.91558
NM_001135115 // Gm12250 // predicted gene 12250 // 11 B1.3|11 // 631323	Gm12250	0.000729117	-4.91256
NM_028935 // Zfp558 // zinc finger protein 558 // 9|9 A3 // 72230 /// XM_006510619 // Z	Zfp558	0.000734403	-4.90742
NR_029457 // G530011O06Rik // RIKEN cDNA G530011O06 gene // X and Y|X // 654820 /// ENS	G530011O06Ri	3.10E-06	-4.89865
---		7.93E-05	-4.89843
NM_009829 // Ccnd2 // cyclin D2 // 6 F3|6 61.92 cM // 12444 /// ENSMUST00000000188 // C	Ccnd2	2.51E-08	-4.88981
---		0.00554253	-4.88745
NM_172734 // Stk38l // serine/threonine kinase 38 like // 6 G3|6 // 232533 /// XM_00650	Stk38l	4.45E-06	-4.88482
NM_007413 // Adora2b // adenosine A2b receptor // 11 B2|11 // 11541 /// ENSMUST00000018	Adora2b	3.31E-05	-4.88111
NM_015783 // Isg15 // ISG15 ubiquitin-like modifier // 4 E2|4 // 100038882 /// ENSMUST0	Isg15	0.00533423	-4.87357
---		0.00512395	-4.85417
ENSMUST00000101477 // Peli1 // pellino 1 // 11 A3.2|11 13.81 cM // 67245 /// AF302503 /	Peli1	6.37E-07	-4.83994

XM_006496589 // LOC101056250 // sp110 nuclear body protein-like // --- // 101056250 ///	LOC101056250	3.98E-05	-4.8312
XM_006535876 // LOC677525 // sp110 nuclear body protein-like // 1|1 // 677525 /// NM_03	LOC677525	3.69E-05	-4.82202
NM_175648 // Trim30b // tripartite motif-containing 30B // 7 E3|7 // 244183 /// ENSMUST	Trim30b	8.67E-05	-4.81769
ENSMUST00000129913 // Igf2bp2 // insulin-like growth factor 2 mRNA binding protein 2 //	Igf2bp2	3.50E-07	-4.80765
NM_001025395 // Src // Rous sarcoma oncogene // 2 H1|2 78.35 cM // 20779 /// NM_009271	Src	2.48E-05	-4.77321
NR_030671 // AW011738 // expressed sequence AW011738 // 4 E2|4 // 100382 /// ENSMUST000	AW011738	0.000975424	-4.77209
NM_001290755 // Tlr7 // toll-like receptor 7 // X F5|X // 170743 /// NM_001290757 // Tl	Tlr7	8.08E-09	-4.76301
NM_001271676 // Ifi47 // interferon gamma inducible protein 47 // 11 B1.2|11 // 15953 /	Ifi47	0.000716896	-4.749
NR_040371 // Gm14023 // predicted gene 14023 // 2|2 62.9 cM // 100503468 /// ENSMUST000	Gm14023	0.000762208	-4.74806
NM_029508 // Pcgf5 // polycomb group ring finger 5 // 19 C2|19 // 76073 /// XM_00652743	Pcgf5	2.85E-05	-4.72256
NM_027711 // Iqgap2 // IQ motif containing GTPase activating protein 2 // 13 D1|13 50.2	Iqgap2	4.66E-07	-4.69286
NM_008329 // Ifi204 // interferon activated gene 204 // 1 H3|1 80.63 cM // 15951 /// XM	Ifi204	0.000624384	-4.68899
BC005693 // Hmgn3 // high mobility group nucleosomal binding domain 3 // 9|9 E3.1 // 94	Hmgn3	6.77E-06	-4.68861
NM_001162925 // Nudt17 // nudix (nucleoside diphosphate linked moiety X)-type motif 17	Nudt17	4.63E-05	-4.68102
ENSMUST00000180798 // Gm26905 // predicted gene, 26905 // --- // ---	Gm26905	0.0046274	-4.67329
NM_011141 // Pou3f1 // POU domain, class 3, transcription factor 1 // 4 D2.2|4 57.86 cM	Pou3f1	0.000148617	-4.64237
ENSMUST00000028141 // 6530402F18Rik // RIKEN cDNA 6530402F18 gene // --- // --- /// ENS	6530402F18Rik	9.53E-06	-4.62851
ENSMUST00000120177 // Gstt1 // glutathione S-transferase, theta 1 // 10 B5-C1|10 38.58	Gstt1	2.87E-06	-4.62694
NR_038025 // 4933412E12Rik // RIKEN cDNA 4933412E12 gene // 10|10 // 71086 /// NR_03802	4933412E12Rik	0.000235683	-4.61796
NM_172203 // Nox1 // NADPH oxidase 1 // X E3|X 55.69 cM // 237038 /// ENSMUST0000003361	Nox1	5.21E-06	-4.6179
NM_019963 // Stat2 // signal transducer and activator of transcription 2 // 10 D3|10 76	Stat2	6.16E-05	-4.61444
NM_011546 // Zeb1 // zinc finger E-box binding homeobox 1 // 18 A1|18 4.42 cM // 21417	Zeb1	9.62E-05	-4.59971
NM_213615 // A530032D15Rik // RIKEN cDNA A530032D15Rik gene // 1 C5|1 // 381287 /// ENS	A530032D15Ril	4.29E-06	-4.59379
ENSMUST00000121995 // Gm15821 // predicted gene 15821 // 17|17 17.98 cM // 100502931 //	Gm15821	4.34E-05	-4.59208
NM_027320 // Ifi35 // interferon-induced protein 35 // 11 D|11 // 70110 /// ENSMUST0000	Ifi35	1.62E-05	-4.58659
NR_002687 // Gm5424 // argininosuccinate synthase pseudogene // 10 B4|10 // 432466 ///	Gm5424	0.000737055	-4.57913
---		0.00435346	-4.56614
XM_006496589 // LOC101056250 // sp110 nuclear body protein-like // --- // 101056250 ///	LOC101056250	1.76E-05	-4.55863
NM_001162412 // Cysltr2 // cysteinyl leukotriene receptor 2 // 14 D3|14 // 70086 /// NM	Cysltr2	1.34E-05	-4.53919
NM_001083927 // Tle3 // transducin-like enhancer of split 3, homolog of Drosophila E(sp	Tle3	1.67E-07	-4.53704
NM_001293635 // Ktn1 // kinectin 1 // 14|14 C2 // 16709 /// NM_001293636 // Ktn1 // kin	Ktn1	9.88E-06	-4.53071
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	3.10E-05	-4.51199
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	3.10E-05	-4.51199
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	3.10E-05	-4.51199
NM_178395 // Zdhhc2 // zinc finger, DHHC domain containing 2 // 8 A4|8 // 70546 /// ENS	Zdhhc2	3.45E-06	-4.50909
NM_008102 // Gch1 // GTP cyclohydrolase 1 // 14 C2-3|14 24.6 cM // 14528 /// ENSMUST000	Gch1	1.93E-06	-4.50362
NM_013875 // Pde7b // phosphodiesterase 7B // 10 A3|10 // 29863 /// XM_006512758 // Pde	Pde7b	1.70E-07	-4.495
NM_023738 // Uba7 // ubiquitin-like modifier activating enzyme 7 // 9 F2|9 59.07 cM //	Uba7	9.97E-07	-4.48413
NM_011530 // Tap2 // transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) // 17	Tap2	1.99E-08	-4.47195
NM_001033632 // Ifitm6 // interferon induced transmembrane protein 6 // 7 F5|7 // 21300	Ifitm6	1.14E-05	-4.47168
XR_378400 // Gm8995 // predicted gene 8995 // 7 E3|7 // 668139 /// ENSMUST00000184842 /	Gm8995	2.21E-05	-4.46867
NM_001008232 // Asap3 // ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 // 4 D3	Asap3	3.74E-07	-4.45294
NM_024495 // Car13 // carbonic anhydrase 13 // 3|3 A2 // 71934 /// ENSMUST00000029071 /	Car13	2.44E-05	-4.44787
NM_001102404 // Acp5 // acid phosphatase 5, tartrate resistant // 9 A3|9 8.38 cM // 114	Acp5	4.62E-06	-4.44028
NM_181402 // Parp11 // poly (ADP-ribose) polymerase family, member 11 // 6 F3|6 // 1011	Parp11	4.46E-06	-4.43825
NR_033498 // AI504432 // expressed sequence AI504432 // 3 F2.3|3 // 229694 /// ENSMUST0	AI504432	0.000751344	-4.43824
---		0.000861093	-4.43551
NM_001013817 // Sp140 // Sp140 nuclear body protein // 1 C5|1 // 434484 /// NM_00103790	Sp140	9.77E-06	-4.43359
NM_001085385 // 1600014C10Rik // RIKEN cDNA 1600014C10 gene // 7|7 B1 // 72244 /// ENSM	1600014C10Rik	6.26E-09	-4.42478
NR_030251 // Mir483 // microRNA 483 // 7|7 // 723874 /// ENSMUST00000093631 // Mir483 /	Mir483	0.000270092	-4.42354
NR_030251 // Mir483 // microRNA 483 // 7|7 // 723874 /// ENSMUST00000093631 // Mir483 /	Mir483	0.000270092	-4.42354
NM_175236 // Adhfe1 // alcohol dehydrogenase, iron containing, 1 // 1 A2|1 // 76187 ///	Adhfe1	9.73E-06	-4.40854
ENSMUST00000157357 // Gm22224 // predicted gene, 22224 // --- // ---	Gm22224	0.0043801	-4.40485
NM_001177881 // Mfap3l // microfibrillar-associated protein 3-like // 8|8 B3.2 // 71306	Mfap3l	4.26E-06	-4.39165
NR_045687 // Gm9895 // predicted gene 9895 // 19 C1|19 // 100503337	Gm9895	4.94E-06	-4.37974
---		0.00109652	-4.37243
XM_006544847 // LOC102642448 // schlafen family member 13-like // --- // 102642448 ///	LOC102642448	4.95E-06	-4.36149
NM_025687 // Tex12 // testis expressed gene 12 // 9 A5.3|9 // 66654 /// ENSMUST00000034	Tex12	0.00160996	-4.3435
NM_008608 // Mmp14 // matrix metallopeptidase 14 (membrane-inserted) // 14 C2|14 27.79	Mmp14	0.000361206	-4.33081
NM_001267583 // Zfp811 // zinc finger protein 811 // 17 B1|17 // 240063 /// NM_183177 /	Zfp811	0.00105391	-4.31184
ENSMUST00000103466 // Ighv11-1 // immunoglobulin heavy variable 11-1 // --- // --- ///	Ighv11-1	0.000151154	-4.28823
NM_008871 // Serpine1 // serine (or cysteine) peptidase inhibitor, clade E, member 1 //	Serpine1	5.11E-06	-4.27429
NM_001289568 // Sass6 // spindle assembly 6 homolog (C. elegans) // 3|3 G2 // 72776 ///	Sass6	5.43E-05	-4.26283
NM_008207 // H2-T24 // histocompatibility 2, T region locus 24 // 17 B1|17 18.84 cM //	H2-T24	6.83E-05	-4.24715
NM_177861 // Tmem67 // transmembrane protein 67 // 4 A1|4 // 329795 /// NR_110955 // Tm	Tmem67	5.78E-06	-4.24565
NR_015474 // Il1bos // interleukin 1 beta, opposite strand // 2 F1|2 // 329514 /// ENSM	Il1bos	0.000260637	-4.23952
NM_001294138 // Gyk // glycerol kinase // X C-D|X 39.32 cM // 14933 /// NM_001294140 //	Gyk	7.22E-06	-4.23646
NR_045657 // 4933432I03Rik // RIKEN cDNA 4933432I03 gene // 14|14 // 71264	4933432I03Rik	0.000153114	-4.23502
ENSMUST00000046739 // Ifi44l // interferon-induced protein 44 like // 3 H3|3 76.94 cM /	Ifi44l	0.000289435	-4.22873
NM_011249 // Rbl1 // retinoblastoma-like 1 (p107) // 2 H1|2 78.05 cM // 19650 /// ENSMU	Rbl1	2.13E-08	-4.22489
NR_110420 // Ptgs2os2 // prostaglandin-endoperoxide synthase 2, opposite strand 2 // 1	Ptgs2os2	8.15E-05	-4.2175
NR_030719 // Gm8979 // very large inducible GTPase 1 pseudogene // 7 E3|7 // 668108 ///	Gm8979	4.74E-05	-4.21646
NM_001170853 // Mndal // myeloid nuclear differentiation antigen like // 1 H3|1 // 1000	Mndal	6.73E-05	-4.2156
NM_001167983 // Sipa1l1 // signal-induced proliferation-associated 1 like 1 // 12 D1|12	Sipa1l1	4.26E-09	-4.21487
---		3.36E-05	-4.20886
NM_009156 // Sepw1 // selenoprotein W, muscle 1 // 7|7 A2 // 20364 /// ENSMUST000000443	Sepw1	1.76E-06	-4.20745
NM_008591 // Met // met proto-oncogene // 6 A2|6 7.83 cM // 17295 /// ENSMUST0000011544	Met	2.76E-05	-4.19892
NM_178732 // Zfp324 // zinc finger protein 324 // 7 A1|7 // 243834 /// ENSMUST000000387	Zfp324	6.36E-05	-4.19159
NM_009141 // Cxcl5 // chemokine (C-X-C motif) ligand 5 // 5 E1|5 44.78 cM // 20311 ///	Cxcl5	0.000537866	-4.1824
NM_198095 // Bst2 // bone marrow stromal cell antigen 2 // 8 B3.3|8 // 69550 /// ENSMUS	Bst2	3.90E-06	-4.18027
NM_011852 // Oas1g // 2-5 oligoadenylate synthetase 1G // 5 F|5 60.65 cM // 23960 /// E	Oas1g	0.000123827	-4.17816
---		0.00545785	-4.17304
NR_030719 // Gm8979 // very large inducible GTPase 1 pseudogene // 7 E3|7 // 668108 ///	Gm8979	6.92E-05	-4.17154
NM_001037713 // Xaf1 // XIAP associated factor 1 // 11 B4|11 // 327959 /// NM_001291153	Xaf1	3.28E-05	-4.16317
NM_001033405 // Treml2 // triggering receptor expressed on myeloid cells-like 2 // 17 C	Treml2	5.23E-05	-4.16294
NM_144559 // Fcgr4 // Fc receptor, IgG, low affinity IV // 1 H3|1 78.53 cM // 246256 //	Fcgr4	3.69E-08	-4.14764
XM_006521741 // Cd86 // CD86 antigen // 16 B5|16 25.72 cM // 12524 /// BC013807 // Cd86	Cd86	0.000115539	-4.14325
NM_001161730 // Tap1 // transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) //	Tap1	5.23E-05	-4.12589
NM_001013368 // E2f8 // E2F transcription factor 8 // 7 B4|7 // 108961 /// ENSMUST00000	E2f8	6.48E-06	-4.11278

ENSMUST00000145914 // Gm15478 // predicted gene 15478 // --- // --- /// AK048962 // Gm1	Gm15478	3.97E-06	-4.11122
NR_029807 // Mir222 // microRNA 222 // X|X // 723828 /// ENSMUST00000083537 // Mir222 /	Mir222	0.000920813	-4.10368
NM_008328 // Ifi203 // interferon activated gene 203 // 1 H3|1 80.76 cM // 15950 /// EN	Ifi203	2.77E-05	-4.07869
NM_001048207 // Gypc // glycophorin C // 18 B1|18 18.05 cM // 71683 /// ENSMUST00000174	Gypc	2.64E-06	-4.0724
---		0.0065885	-4.06973
NM_001256096 // Dtx2 // deltex 2 homolog (Drosophila) // 5 G2|5 // 74198 /// NM_0012560	Dtx2	0.000178182	-4.06851
---		0.00668499	-4.06373
NM_001163575 // Parp10 // poly (ADP-ribose) polymerase family, member 10 // 15 D3|15 //	Parp10	2.67E-06	-4.04783
NM_011409 // Slfn3 // schlafen 3 // 11 C|11 // 20557 /// XM_006532656 // Slfn3 // schla	Slfn3	2.69E-05	-4.04706
AK089726 // Trim30a // tripartite motif-containing 30A // 7 E3|7 55.69 cM // 20128	Trim30a	0.000510591	-4.04626
---		0.00392912	-4.04104
NM_175523 // Ppm1k // protein phosphatase 1K (PP2C domain containing) // 6 B3|6 // 2433	Ppm1k	1.84E-05	-4.0145
NM_001290801 // Mgat4a // mannoside acetylglucosaminyltransferase 4, isoenzyme A // 1 B	Mgat4a	3.20E-05	-3.99824
NM_013531 // Gnb4 // guanine nucleotide binding protein (G protein), beta 4 // 3|3 B //	Gnb4	3.02E-06	-3.98418
NM_009871 // Cdk5r1 // cyclin-dependent kinase 5, regulatory subunit 1 (p35) // 11 B5|1	Cdk5r1	8.02E-05	-3.96703
NM_001048177 // Jak2 // Janus kinase 2 // 19 C1|19 23.73 cM // 16452 /// NM_008413 // J	Jak2	0.000239512	-3.96316
NM_009767 // Chic1 // cysteine-rich hydrophobic domain 1 // X D|X 42.3 cM // 12212 ///	Chic1	7.24E-06	-3.959
NR_108021 // Gm16712 // predicted gene, 16712 // 17|17 29.08 cM // 100504333 /// ENSMUS	Gm16712	0.000228532	-3.9501
ENSMUST00000174654 // Gm20470 // predicted gene 20470 // --- // --- /// AK132823 // Kat	Gm20470	8.13E-05	-3.94079
---		0.00275342	-3.92917
NM_016979 // Prkx // protein kinase, X-linked // X A7.3|X // 19108 /// XM_006527909 //	Prkx	3.47E-07	-3.92903
NM_001161790 // Mefv // Mediterranean fever // 16 A1|16 2.18 cM // 54483 /// NM_0011617	Mefv	0.00611593	-3.92723
NM_001013817 // Sp140 // Sp140 nuclear body protein // 1 C5|1 // 434484 /// ENSMUST0000	Sp140	0.00177009	-3.92169
ENSMUST00000111314 // Adamts4 // a disintegrin-like and metallopeptidase (reprolysin ty	Adamts4	0.000442148	-3.91309
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	9.62E-06	-3.89569
NM_145949 // Ido2 // indoleamine 2,3-dioxygenase 2 // 8 A2|8 // 209176 /// ENSMUST00000	Ido2	6.27E-05	-3.88232
NM_001267621 // Gfi1 // growth factor independent 1 // 5 F|5 52.23 cM // 14581 /// NM_0	Gfi1	4.83E-05	-3.8822
NM_145944 // Ccdc25 // coiled-coil domain containing 25 // 14 D1|14 // 67179 /// ENSMUS	Ccdc25	0.000147717	-3.8766
NM_198862 // Nlgn2 // neuroligin 2 // 11 B3|11 // 216856 /// ENSMUST00000056484 // Nlgn	Nlgn2	6.77E-06	-3.86487
---		0.00599608	-3.86246
NM_133948 // Psip1 // PC4 and SFRS1 interacting protein 1 // 4 C3|4 // 101739 /// ENSMU	Psip1	1.80E-07	-3.85946
NM_001033136 // Rmdn3 // regulator of microtubule dynamics 3 // 2 E5|2 // 67809 /// ENS	Rmdn3	1.63E-06	-3.85623
NM_028270 // Aldh1b1 // aldehyde dehydrogenase 1 family, member B1 // 4|4 B2 // 72535 /	Aldh1b1	4.16E-05	-3.83789
NM_172659 // Slc2a6 // solute carrier family 2 (facilitated glucose transporter), membe	Slc2a6	0.00335899	-3.83727
NM_030150 // Dhx58 // DEXH (Asp-Glu-X-His) box polypeptide 58 // 11 D|11 63.52 cM // 80	Dhx58	6.29E-06	-3.83125
---		0.00387615	-3.82845
---		0.00387615	-3.82845
NM_001113379 // Lrrc32 // leucine rich repeat containing 32 // 7 E2|7 53.86 cM // 43421	Lrrc32	1.97E-05	-3.81242
NM_001033759 // Tmem2 // transmembrane protein 2 // 19 B|19 // 83921 /// NM_031997 // T	Tmem2	4.60E-07	-3.80899
NM_007865 // Dll1 // delta-like 1 (Drosophila) // 17 A2|17 8.95 cM // 13388 /// XM_0065	Dll1	0.000365618	-3.79213
NM_207244 // Cd200r4 // CD200 receptor 4 // 16 B4|16 // 239849 /// XM_006522128 // Cd20	Cd200r4	3.59E-08	-3.79088
---		0.00529187	-3.79062
---		2.37E-05	-3.78994
NM_001163590 // Stx11 // syntaxin 11 // 10 A1|10 // 74732 /// NM_029075 // Stx11 // syn	Stx11	7.99E-05	-3.78563
---		7.78E-05	-3.77007
NM_007936 // Epha4 // Eph receptor A4 // 1 C1-C5|1 39.55 cM // 13838 /// ENSMUST0000002	Epha4	4.05E-05	-3.76892
---		0.00563992	-3.768
NM_153510 // Pilra // paired immunoglobin-like type 2 receptor alpha // 5 G2|5 // 23180	Pilra	1.03E-05	-3.76014
NM_001040026 // Sco1 // SCO cytochrome oxidase deficient homolog 1 (yeast) // 11 B3|11	Sco1	3.68E-06	-3.75012
---		5.61E-05	-3.74479
NM_009403 // Tnfsf8 // tumor necrosis factor (ligand) superfamily, member 8 // 4 C1|4 3	Tnfsf8	9.19E-06	-3.74418
NM_001037294 // Alpk2 // alpha-kinase 2 // 18 E1|18 // 225638 /// ENSMUST00000035548 //	Alpk2	3.37E-06	-3.73747
NM_008842 // Pim1 // proviral integration site 1 // 17 A3.3|17 15.38 cM // 18712 /// EN	Pim1	2.99E-05	-3.72892
NM_175118 // Dusp28 // dual specificity phosphatase 28 // 1 D|1 // 67446 /// ENSMUST000	Dusp28	7.85E-05	-3.72886
NM_017466 // Ccrl2 // chemokine (C-C motif) receptor-like 2 // 9 F|9 60.92 cM // 54199	Ccrl2	0.000331314	-3.72793
NM_011633 // Traf5 // TNF receptor-associated factor 5 // 1 H6|1 97.11 cM // 22033 ///	Traf5	1.01E-05	-3.72592
NM_001289617 // Zyx // zyxin // 6 B2.1|6 // 22793 /// NM_001289619 // Zyx // zyxin // 6	Zyx	1.76E-06	-3.71016
---		4.97E-07	-3.70834
---		0.00189761	-3.70773
NM_001190400 // Bend7 // BEN domain containing 7 // 2 A1|2 // 209645 /// NM_178663 // B	Bend7	0.00032662	-3.70241
NM_028523 // Dcbld2 // discoidin, CUB and LCCL domain containing 2 // 16 C1.2|16 // 733	Dcbld2	5.20E-05	-3.69869
NM_001083616 // Cacna1d // calcium channel, voltage-dependent, L type, alpha 1D subunit	Cacna1d	8.94E-06	-3.68725
NM_030098 // Rnase6 // ribonuclease, RNase A family, 6 // 14 C1|14 // 78416 /// ENSMUST	Rnase6	2.23E-06	-3.67559
NM_021887 // Il21r // interleukin 21 receptor // 7|7 F4 // 60504 /// XM_006508097 // Il	Il21r	2.74E-07	-3.66483
NR_045367 // A630012P03Rik // RIKEN cDNA A630012P03 gene // X A5|X // 100504594 /// ENS	A630012P03Rik	3.02E-05	-3.66089
NM_027182 // Trip13 // thyroid hormone receptor interactor 13 // 13 C1|13 40.15 cM // 6	Trip13	2.55E-06	-3.65132
ENSMUST00000160674 // Csprs // component of Sp100-rs // 8 B1.3|1 // 114564 /// ENSMUST0	Csprs	5.17E-05	-3.6468
NM_008326 // Irgm1 // immunity-related GTPase family M member 1 // 11 B1.2|11 // 15944	Irgm1	2.29E-05	-3.63918
ENSMUST00000139725 // Mitd1 // MIT, microtubule interacting and transport, domain conta	Mitd1	5.41E-06	-3.61858
ENSMUST00000071792 // 1110038F14Rik // RIKEN cDNA 1110038F14 gene // 15|15 E1 // 117171	1110038F14Rik	2.36E-06	-3.59961
NM_001169131 // Papd7 // PAP associated domain containing 7 // 13 C1|13 35.55 cM // 210	Papd7	1.14E-05	-3.59615
NM_001190846 // Kat2b // K(lysine) acetyltransferase 2B // 17 C|17 27.86 cM // 18519 //	Kat2b	1.39E-05	-3.59283
NM_011267 // Rgs16 // regulator of G-protein signaling 16 // 1 G3|1 65.43 cM // 19734 /	Rgs16	2.49E-05	-3.59276
NM_009223 // Snn // stannin // 16|16 A2 // 20621 /// ENSMUST00000089011 // Snn // stann	Snn	2.05E-05	-3.58395
ENSMUST00000136542 // Gm11772 // predicted gene 11772 // --- // ---	Gm11772	0.000459847	-3.58012
NM_172883 // Mfsd7a // major facilitator superfamily domain containing 7A // 5 F|5 // 2	Mfsd7a	1.65E-05	-3.57876
NM_010398 // H2-T23 // histocompatibility 2, T region locus 23 // 17 B1|17 18.86 cM //	H2-T23	6.06E-06	-3.57303
NM_138682 // Lrrc4 // leucine rich repeat containing 4 // 6 A3.3|6 // 192198 /// ENSMUS	Lrrc4	0.000131967	-3.57163
NM_001004185 // Whamm // WAS protein homolog associated with actin, golgi membranes and	Whamm	4.40E-07	-3.57055
XM_006537281 // Psmb9 // proteasome (prosome, macropain) subunit, beta type 9 (large mu	Psmb9	4.66E-06	-3.56895
NM_001034909 // Gm6034 // predicted gene 6034 // 17 B1|17 // 547347 /// ENSMUST00000097	Gm6034	0.000760847	-3.56105
NM_010426 // Foxf1 // forkhead box F1 // 8 E1|8 70.31 cM // 15227 /// ENSMUST0000018150	Foxf1	0.00256245	-3.55747
---		0.00414304	-3.55277
NM_172893 // Parp12 // poly (ADP-ribose) polymerase family, member 12 // 6 B1|6 // 2437	Parp12	8.02E-05	-3.55152
NM_001005863 // Mtus1 // mitochondrial tumor suppressor 1 // 8 A4|8 // 102103 /// NM_00	Mtus1	7.44E-06	-3.5477
---		0.00633483	-3.54407
NM_026384 // Dgat2 // diacylglycerol O-acyltransferase 2 // 7|7 F1 // 67800 /// ENSMUST	Dgat2	0.000131691	-3.53457
ENSMUST00000122664 // n-R5s164 // nuclear encoded rRNA 5S 164 // --- // ---	n-R5s164	0.00651714	-3.52837
NM_001077189 // Fcgr2b // Fc receptor, IgG, low affinity IIb // 1 H3|1 78.02 cM // 1413	Fcgr2b	5.55E-07	-3.52699

---		4.23E-05	-3.52631
NM_177034 // Apba1 // amyloid beta (A4) precursor protein binding, family A, member 1 /	Apba1	4.47E-07	-3.5261
NM_001045481 // Ifi203 // interferon activated gene 203 // 1 H3|1 80.76 cM // 15950 ///	Ifi203	1.46E-05	-3.51904
NM_001029984 // Fcrlb // Fc receptor-like B // 1 H3|1 // 435653 /// ENSMUST00000094337	Fcrlb	0.00120184	-3.50051
---		0.000979206	-3.49865
ENSMUST00000142107 // Gm11626 // predicted gene 11626 // --- // ---	Gm11626	0.00159462	-3.49577
NM_009775 // Tspo // translocator protein // 15 E1|15 39.4 cM // 12257 /// ENSMUST00000	Tspo	7.77E-06	-3.49272
NM_001198560 // H2-Q7 // histocompatibility 2, Q region locus 7 // 17 B1|17 18.67 cM //	H2-Q7	0.00325206	-3.49216
NM_145857 // Nod2 // nucleotide-binding oligomerization domain containing 2 // 8 C3|8 /	Nod2	1.78E-05	-3.4916
XM_006497081 // Gm16340 // predicted gene 16340 // 1|1 80.65 cM // 100504287 /// ENSMUS	Gm16340	0.000244488	-3.49059
NM_011332 // Ccl17 // chemokine (C-C motif) ligand 17 // 8 C5|8 46.85 cM // 20295 /// X	Ccl17	0.00117385	-3.48474
NM_001177602 // Ak4 // adenylate kinase 4 // 4 C6|4 46.84 cM // 11639 /// XM_006502684	Ak4	9.73E-06	-3.47559
NM_001252503 // Aftph // aftiphilin // 11 A3.1|11 // 216549 /// NM_001290545 // Aftph /	Aftph	5.66E-06	-3.47424
NM_194346 // Rnf31 // ring finger protein 31 // 14 C3|14 // 268749 /// ENSMUST000000194	Rnf31	2.30E-06	-3.46745
NM_025653 // 3110001I22Rik // RIKEN cDNA 3110001I22 gene // 16 A1|16 // 66598 /// NM_02	3110001I22Rik	7.49E-07	-3.46337
---		0.000981309	-3.46272
NM_008327 // Ifi202b // interferon activated gene 202B // 1 H3|1 // 26388 /// NM_011940	Ifi202b	5.52E-05	-3.45974
NR_040335 // D330050G23Rik // RIKEN cDNA D330050G23 gene // 2|2 // 320975 /// ENSMUST00	D330050G23Ril	8.48E-06	-3.45207
NM_029250 // Etnk1 // ethanolamine kinase 1 // 6 G3|6 75.41 cM // 75320 /// ENSMUST0000	Etnk1	6.79E-07	-3.44906
XR_401026 // A730011C13Rik // RIKEN cDNA A730011C13 gene // 3|3 // 319916 /// ENSMUST00	A730011C13Rik	7.36E-06	-3.44766
ENSMUST00000104150 // Gm23294 // predicted gene, 23294 // --- // ---	Gm23294	0.000214984	-3.43798
NM_133954 // Usb1 // U6 snRNA biogenesis 1 // 8 D1|8 // 101985 /// ENSMUST00000034245 /	Usb1	2.13E-06	-3.43427
NM_011345 // Sele // selectin, endothelial cell // 1 H2.2|1 71.35 cM // 20339 /// ENSMU	Sele	0.000370597	-3.43261
NM_009022 // Aldh1a2 // aldehyde dehydrogenase family 1, subfamily A2 // 9 D|9 39.85 cM	Aldh1a2	8.13E-05	-3.43052
NM_001271375 // Milr1 // mast cell immunoglobulin like receptor 1 // 11 E1|11 // 380732	Milr1	6.44E-06	-3.42807
NM_001122680 // Pvrl4 // poliovirus receptor-related 4 // 1 H2|1 // 71740 /// NM_027893	Pvrl4	1.28E-05	-3.42304
ENSMUST00000170385 // Ighd6-1 // immunoglobulin heavy diversity 6-1 // --- // --- /// E	Ighd6-1	0.00584786	-3.4189
ENSMUST00000170385 // Ighd6-1 // immunoglobulin heavy diversity 6-1 // --- // --- /// E	Ighd6-1	0.00584786	-3.4189
NM_145458 // Pxk // PX domain containing serine/threonine kinase // 14 A1|14 4.7 cM //	Pxk	7.97E-09	-3.40909
NR_045324 // Gm19705 // predicted gene, 19705 // 1 E4-F|1 59.94 cM // 100503460 /// NR_	Gm19705	0.000273411	-3.40608
NM_001009940 // Il19 // interleukin 19 // 1 E4|1 // 329244 /// ENSMUST00000016668 // Il	Il19	2.27E-05	-3.39631
NM_013754 // Insl6 // insulin-like 6 // 19|19 C3 // 27356 /// ENSMUST00000052380 // Ins	Insl6	1.71E-05	-3.39599
---		1.89E-05	-3.38964
AK032092 // Sh3bgrl2 // SH3 domain binding glutamic acid-rich protein like 2 // 9 E2|9	Sh3bgrl2	1.35E-05	-3.38731
NM_010186 // Fcgr1 // Fc receptor, IgG, high affinity I // 3 F2.1|3 41.72 cM // 14129 /	Fcgr1	7.55E-07	-3.38617
ENSMUST00000120059 // Gm5388 // predicted gene 5388 // --- // --- /// ENSMUST0000017552	Gm5388	0.00238214	-3.38566
NM_145968 // Tagap // T cell activation Rho GTPase activating protein // 17 A1|17 // 72	Tagap	0.000563507	-3.38396
NM_172409 // Fmnl2 // formin-like 2 // 2 C1.1|2 // 71409 /// XM_006498332 // Fmnl2 // f	Fmnl2	3.80E-05	-3.37806
NM_010531 // Il18bp // interleukin 18 binding protein // 7|7 F1 // 16068 /// ENSMUST000	Il18bp	6.61E-06	-3.37765
AK035387 // Gm20559 // predicted gene, 20559 // 6 A1|6 // 330256	Gm20559	8.13E-06	-3.37511
NR_029806 // Mir221 // microRNA 221 // X|X // 723827 /// ENSMUST00000083488 // Mir221 /	Mir221	4.85E-05	-3.36949
NM_030253 // Parp9 // poly (ADP-ribose) polymerase family, member 9 // 16 B3|16 // 8028	Parp9	4.35E-06	-3.36937
NM_001284409 // Casp3 // caspase 3 // 8 B1.1|8 26.39 cM // 12367 /// NM_009810 // Casp3	Casp3	2.07E-05	-3.3688
NM_001122675 // Zcchc2 // zinc finger, CCHC domain containing 2 // 1 E2.1|1 // 227449 /	Zcchc2	2.22E-05	-3.35989
NM_172812 // Htr2a // 5-hydroxytryptamine (serotonin) receptor 2A // 14 D2|14 39.37 cM	Htr2a	0.000143057	-3.35961
NR_045641 // F630111L10Rik // RIKEN cDNA F630111L10 gene // 3 D|3 // 320463 /// AK17084	F630111L10Rik	2.49E-06	-3.35715
---		0.000320498	-3.35654
NM_133990 // Il13ra1 // interleukin 13 receptor, alpha 1 // X A3.3|X 20.49 cM // 16164	Il13ra1	5.01E-06	-3.35201
NM_001040399 // Larp1b // La ribonucleoprotein domain family, member 1B // 3 B|3 // 214	Larp1b	0.000581695	-3.34336
NM_013673 // Sp100 // nuclear antigen Sp100 // 1 C5|1 43.6 cM // 20684 /// XM_006529287	Sp100	2.98E-05	-3.34278
---		0.00315782	-3.32797
---		0.00010688	-3.31364
NM_021457 // Fzd1 // frizzled homolog 1 (Drosophila) // 5 A1|5 2.61 cM // 14362 /// ENS	Fzd1	0.000118896	-3.30526
NM_001110824 // Foxp4 // forkhead box P4 // 17 C|17 // 74123 /// NM_001110825 // Foxp4	Foxp4	0.000233544	-3.30262
ENSMUST00000093902 // Rnf213 // ring finger protein 213 // 11 E2|11 83.48 cM // 672511	Rnf213	0.000708944	-3.30192
NM_007609 // Casp4 // caspase 4, apoptosis-related cysteine peptidase // 9 A1|9 2.46 cM	Casp4	0.000385371	-3.30165
---		2.06E-05	-3.30089
NM_027309 // Lysmd2 // LysM, putative peptidoglycan-binding, domain containing 2 // 9 D	Lysmd2	1.58E-05	-3.29962
NM_010484 // Slc6a4 // solute carrier family 6 (neurotransmitter transporter, serotonin	Slc6a4	9.65E-06	-3.29811
NM_001204910 // AI607873 // expressed sequence AI607873 // 1 H3|1 // 226691 /// ENSMUST	AI607873	0.000576016	-3.29507
NM_032396 // Kremen1 // kringle containing transmembrane protein 1 // 11 A1|11 // 84035	Kremen1	1.93E-05	-3.28598
NM_028044 // Cnn3 // calponin 3, acidic // 3 G1|3 // 71994 /// ENSMUST00000029773 // Cn	Cnn3	5.76E-08	-3.28496
NM_001164202 // Gm8369 // predicted gene 8369 // 19 A|19 // 666926 /// XM_006527260 //	Gm8369	0.00141198	-3.27457
NM_001077509 // Tnfrsf9 // tumor necrosis factor receptor superfamily, member 9 // 4 E2	Tnfrsf9	0.000589909	-3.27292
NR_045813 // 4930599N23Rik // RIKEN cDNA 4930599N23 gene // 6 B1|6 // 75379 /// ENSMUST	4930599N23Ril	0.00194008	-3.26974
ENSMUST00000143099 // 6530409C15Rik // RIKEN cDNA 6530409C15 gene // 6 A3.2|6 // 76224	6530409C15Rik	0.000625762	-3.26855
NM_001114679 // 9930111J21Rik1 // RIKEN cDNA 9930111J21 gene 1 // 11 B1.2|11 // 667214	9930111J21Rik	2.30E-05	-3.25784
NM_016811 // Dgka // diacylglycerol kinase, alpha // 10 D3|10 77.14 cM // 13139 /// XM_	Dgka	3.85E-07	-3.2503
NM_001035228 // St3gal5 // ST3 beta-galactoside alpha-2,3-sialyltransferase 5 // 6|6 C3	St3gal5	9.63E-07	-3.24967
NM_007808 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063 /// ENSMUST000	Cycs	4.43E-05	-3.2407
NM_007808 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063 /// ENSMUST000	Cycs	4.43E-05	-3.2407
NM_172689 // Ddx58 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 // 4 A5|4 // 230073 ///	Ddx58	0.000125999	-3.24043
ENSMUST00000141700 // Gm15987 // predicted gene 15987 // 6|6 63.11 cM // 100504591 ///	Gm15987	0.000615914	-3.23461
NM_001004157 // Scarf1 // scavenger receptor class F, member 1 // 11 B5|11 // 380713 //	Scarf1	0.000115465	-3.2312
NM_172697 // Prpf38a // PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	Prpf38a	3.46E-06	-3.2307
NM_134102 // Pla1a // phospholipase A1 member A // 16 B4|16 26.83 cM // 85031 /// XM_00	Pla1a	0.000873725	-3.22399
XM_006533108 // Rhbdf2 // rhomboid 5 homolog 2 (Drosophila) // 11 E2|11 // 217344 /// E	Rhbdf2	2.88E-06	-3.22034
NM_001143689 // H2-Q4 // histocompatibility 2, Q region locus 4 // 17 B1|17 18.65 cM //	H2-Q4	0.000105771	-3.21475
NR_033804 // Art2a-ps // ADP-ribosyltransferase 2a, pseudogene // 7 E3|7 54.6 cM // 118	Art2a-ps	0.000429599	-3.20972
NM_029084 // Slamf8 // SLAM family member 8 // 1|1 H2 // 74748 /// ENSMUST00000065679 /	Slamf8	0.000133449	-3.20908
NM_172413 // Rap2c // RAP2C, member of RAS oncogene family // X A5|X // 72065 /// ENSMU	Rap2c	6.84E-06	-3.20633
NM_001048054 // Dusp16 // dual specificity phosphatase 16 // 6 G1|6 65.77 cM // 70686 /	Dusp16	9.76E-06	-3.18591
NM_019949 // Ube2l6 // ubiquitin-conjugating enzyme E2L 6 // 2|2 E1 // 56791 /// ENSMUS	Ube2l6	3.43E-05	-3.18457
NM_028287 // Zufsp // zinc finger with UFM1-specific peptidase domain // 10 B1|10 // 72	Zufsp	4.63E-07	-3.18412
NM_175256 // Heg1 // HEG homolog 1 (zebrafish) // 16 B3|16 // 77446 /// XM_006522719 //	Heg1	2.50E-05	-3.17632
XM_006528554 // Armcx6 // armadillo repeat containing, X-linked 6 // X E3|X // 278097 /	Armcx6	3.19E-05	-3.17292
NM_145391 // Tapbpl // TAP binding protein-like // 6 F3|6 // 213233 /// XM_006505862 //	Tapbpl	0.000267526	-3.16457
XM_006505152 // Zfp800 // zinc finger protein 800 // 6 A3.2|6 // 627049 /// ENSMUST0000	Zfp800	5.36E-06	-3.16083
NM_001166402 // Tnfaip3 // tumor necrosis factor, alpha-induced protein 3 // 10 A3|10 8	Tnfaip3	0.00179973	-3.15947

NM_001012236 // Trex1 // three prime repair exonuclease 1 // 9 F2|9 // 22040 /// NM_011	Trex1	5.91E-05	-3.1579
NM_001033450 // Mnda // myeloid cell nuclear differentiation antigen // 1 H3|1 // 38130	Mnda	0.00166299	-3.15542
---		0.00506365	-3.15449
NM_001164071 // Tank // TRAF family member-associated Nf-kappa B activator // 2 C1.3|2	Tank	4.80E-06	-3.15432
ENSMUST00000154924 // Pnpt1 // polyribonucleotide nucleotidyltransferase 1 // 11|11 A4	Pnpt1	6.31E-07	-3.15185
NM_033322 // Lztfl1 // leucine zipper transcription factor-like 1 // 9 F|9 74.36 cM //	Lztfl1	4.13E-05	-3.1475
NM_011113 // Plaur // plasminogen activator, urokinase receptor // 7 A3|7 // 18793 ///	Plaur	1.45E-06	-3.14472
NM_145211 // Oas1a // 2-5 oligoadenylate synthetase 1A // 5 F|5 60.65 cM // 246730 ///	Oas1a	0.000251383	-3.14027
NM_183249 // Wfdc21 // WAP four-disulfide core domain 21 // 11 C|11 // 66107 /// ENSMUS	Wfdc21	0.000193247	-3.13731
NM_172393 // Aim1 // absent in melanoma 1 // 10 B2|10 23.14 cM // 11630 /// ENSMUST0000	Aim1	7.74E-07	-3.13414
NM_010577 // Itga5 // integrin alpha 5 (fibronectin receptor alpha) // 15 F3|15 58.9 cM	Itga5	5.53E-05	-3.12922
NM_133921 // Nfxl1 // nuclear transcription factor, X-box binding-like 1 // 5|5 D // 10	Nfxl1	6.06E-06	-3.12885
NM_007832 // Dck // deoxycytidine kinase // 5 E2|5 // 13178 /// ENSMUST00000031311 // D	Dck	1.68E-05	-3.12427
NM_010404 // Hap1 // huntingtin-associated protein 1 // 11 D|11 63.47 cM // 15114 /// N	Hap1	1.36E-05	-3.12275
NM_001168334 // Gm2799 // predicted gene 2799 // X A3.1|X // 100040482 /// ENSMUST00000	Gm2799	0.000302876	-3.10997
NM_001160018 // Tor1aip1 // torsin A interacting protein 1 // 1 G3|1 // 208263 /// NM_0	Tor1aip1	6.32E-05	-3.10815
NM_133821 // Phlpp1 // PH domain and leucine rich repeat protein phosphatase 1 // 1 E2.	Phlpp1	1.22E-05	-3.10664
NM_133737 // Lancl2 // LanC (bacterial lantibiotic synthetase component C)-like 2 // 6|	Lancl2	1.51E-05	-3.10183
ENSMUST00000116345 // Gm17193 // predicted gene 17193 // --- // ---	Gm17193	6.99E-05	-3.09737
NR_015514 // 9330175E14Rik // RIKEN cDNA 9330175E14 gene // 8 C5|8 // 320377 /// ENSMUS	9330175E14Rik	0.00098427	-3.08617
NM_175088 // Mdfic // MyoD family inhibitor domain containing // 6 A1|6 // 16543 /// EN	Mdfic	1.33E-06	-3.0789
NR_024017 // 4930594C11Rik // G1 to S phase transition pseudogene // 1 B|1 // 77633	4930594C11Rik	0.0033487	-3.078
NM_013673 // Sp100 // nuclear antigen Sp100 // 1 C5|1 43.6 cM // 20684 /// XM_006529287	Sp100	9.94E-06	-3.0719
NM_145227 // Oas2 // 2-5 oligoadenylate synthetase 2 // 5 F|5 60.64 cM // 246728 /// XM	Oas2	2.73E-05	-3.07071
NM_172722 // Naa25 // N(alpha)-acetyltransferase 25, NatB auxiliary subunit // 5 F|5 //	Naa25	1.01E-07	-3.06807
NM_028440 // Abracl // ABRA C-terminal like // 10 A3|10 // 73112 /// ENSMUST00000020002	Abracl	3.42E-05	-3.06498
NM_138657 // Socs7 // suppressor of cytokine signaling 7 // 11 D|11 // 192157 /// XM_00	Socs7	4.63E-05	-3.06329
NM_001130476 // Tpst1 // protein-tyrosine sulfotransferase 1 // 5|5 F-G1 // 22021 /// N	Tpst1	0.000344248	-3.06023
NM_001159543 // Dpp4 // dipeptidylpeptidase 4 // 2 C2-D|2 35.85 cM // 13482 /// NM_0100	Dpp4	0.00230129	-3.05845
XM_006543523 // Gm7160 // predicted gene 7160 // 1 E2.1|1 // 635504	Gm7160	0.000179035	-3.05459
ENSMUST00000111276 // Slamf7 // SLAM family member 7 // 1|1 H2 // 75345 /// AB196816 //	Slamf7	5.48E-05	-3.05133
ENSMUST00000125475 // Fam3b // family with sequence similarity 3, member B // 16 C4|16	Fam3b	2.45E-05	-3.04506
NM_001135151 // Slc39a14 // solute carrier family 39 (zinc transporter), member 14 // 1	Slc39a14	4.33E-05	-3.04151
NM_001033308 // Themis2 // thymocyte selection associated family member 2 // 4 D2.3|4 /	Themis2	1.10E-07	-3.04032
---		0.00665058	-3.03969
NM_001146348 // Eng // endoglin // 2 B|2 22.09 cM // 13805 /// NM_001146350 // Eng // e	Eng	2.01E-06	-3.03803
NM_029522 // Gpsm2 // G-protein signalling modulator 2 (AGS3-like, C. elegans) // 3 F3|	Gpsm2	1.18E-05	-3.0354
NM_011979 // Vnn3 // vanin 3 // 10 A2-B1|10 // 26464 /// ENSMUST00000020190 // Vnn3 //	Vnn3	0.000325013	-3.03352
NM_145523 // Gca // grancalcin // 2 C1.3|2 // 227960 /// ENSMUST00000028257 // Gca // g	Gca	0.00101159	-3.02332
NR_030440 // Mir674 // microRNA 674 // 2|2 // 732489 /// ENSMUST00000102421 // Mir674 /	Mir674	0.000988427	-3.02093
NM_029509 // Gbp8 // guanylate-binding protein 8 // 5 E5|5 // 76074 /// ENSMUST00000031	Gbp8	0.00039846	-3.02072
NM_174850 // Micall2 // MICAL-like 2 // 5 G2|5 // 231830 /// ENSMUST00000044642 // Mica	Micall2	0.00067038	-3.0133
NM_001172160 // Flrt3 // fibronectin leucine rich transmembrane protein 3 // 2 F3|2 //	Flrt3	0.00310483	-3.01089
NM_007984 // Fscn1 // fascin homolog 1, actin bundling protein (Strongylocentrotus purp	Fscn1	2.20E-05	-3.00947
NM_009627 // Adm // adrenomedullin // 7 F1|7 57.7 cM // 11535 /// ENSMUST00000033054 //	Adm	0.00126378	-3.00921
NM_010585 // Itpr1 // inositol 1,4,5-trisphosphate receptor 1 // 6 E1-E2|6 49.74 cM //	Itpr1	4.00E-06	-3.00803
NM_001045540 // Gm12185 // predicted gene 12185 // 11 B1.2|11 // 620913 /// ENSMUST0000	Gm12185	0.00369464	-2.99914
ENSMUST00000101295 // 9930111J21Rik2 // RIKEN cDNA 9930111J21 gene 2 // 11 B1.2|11 // 2	9930111J21Rik	0.000294653	-2.9987
NM_016846 // Rgl1 // ral guanine nucleotide dissociation stimulator,-like 1 // 1|1 G2 /	Rgl1	2.18E-05	-2.99596
NM_001005421 // Amica1 // adhesion molecule, interacts with CXADR antigen 1 // 9 A5.2|9	Amica1	1.48E-05	-2.98654
NM_019423 // Elovl2 // elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3,	Elovl2	1.83E-05	-2.98557
NM_172833 // Malt1 // mucosa associated lymphoid tissue lymphoma translocation gene 1 /	Malt1	0.00460151	-2.98259
NM_138952 // Ripk2 // receptor (TNFRSF)-interacting serine-threonine kinase 2 // 4 A2|4	Ripk2	4.75E-06	-2.98068
NM_011163 // Eif2ak2 // eukaryotic translation initiation factor 2-alpha kinase 2 // 17	Eif2ak2	0.000168502	-2.9783
---		0.00143152	-2.97767
ENSMUST00000144738 // Gm15726 // predicted gene 15726 // --- // ---	Gm15726	2.04E-05	-2.9766
ENSMUST00000181307 // Gm26902 // predicted gene, 26902 // --- // --- /// ENSMUST0000018	Gm26902	0.00356654	-2.97534
NM_001040699 // Mtmr7 // myotubularin related protein 7 // 8|8 B1.2 // 54384 /// ENSMUS	Mtmr7	3.15E-05	-2.97488
NM_175687 // A230050P20Rik // RIKEN cDNA A230050P20 gene // 9 A3|9 // 319278 /// ENSMUS	A230050P20Rik	3.02E-05	-2.97309
NM_001267724 // Asb13 // ankyrin repeat and SOCS box-containing 13 // 13 A1|13 // 14268	Asb13	5.61E-06	-2.97173
NM_173370 // Cds1 // CDP-diacylglycerol synthase 1 // 5 E4|5 // 74596 /// ENSMUST000000	Cds1	2.31E-06	-2.97152
NM_178892 // Tiparp // TCDD-inducible poly(ADP-ribose) polymerase // 3 E1|3 // 99929 //	Tiparp	1.09E-05	-2.96317
NM_027490 // Dcp2 // DCP2 decapping enzyme homolog (S. cerevisiae) // 18 B3|18 // 70640	Dcp2	2.54E-05	-2.95816
NM_027482 // 5730508B09Rik // RIKEN cDNA 5730508B09 gene // 3|3 H1 // 70617 /// ENSMUST	5730508B09Rik	0.00279222	-2.95267
ENSMUST00000180685 // Gm26797 // predicted gene, 26797 // --- // ---	Gm26797	0.00170428	-2.9513
NM_001281934 // Pcsk7 // proprotein convertase subtilisin/kexin type 7 // 9 A5.2|9 25.3	Pcsk7	4.58E-05	-2.94543
NM_011486 // Stat3 // signal transducer and activator of transcription 3 // 11 D|11 63.	Stat3	2.48E-06	-2.94543
NM_001081549 // Rcan1 // regulator of calcineurin 1 // 16 C4|16 53.6 cM // 54720 /// NM	Rcan1	3.51E-06	-2.94509
---		0.00610434	-2.94443
NM_023182 // Ctrl // chymotrypsin-like // 8 D3|8 53.06 cM // 109660 /// ENSMUST00000034	Ctrl	0.000585495	-2.94363
NM_028603 // Zbtb8a // zinc finger and BTB domain containing 8a // 4 D2.2|4 // 73680 //	Zbtb8a	2.05E-06	-2.94327
ENSMUST00000110005 // Rin2 // Ras and Rab interactor 2 // 2 G1|2 // 74030 /// NM_028724	Rin2	4.29E-06	-2.94181
NM_011835 // Katna1 // katanin p60 (ATPase-containing) subunit A1 // 10 A1|10 // 23924	Katna1	0.00236137	-2.93424
NM_016758 // Rgs14 // regulator of G-protein signaling 14 // 13 B1|13 29.8 cM // 51791	Rgs14	0.000261458	-2.92946
NM_178644 // Oaf // OAF homolog (Drosophila) // 9 A5.1|9 24.24 cM // 102644 /// ENSMUST	Oaf	0.000100199	-2.92904
NM_011854 // Oasl2 // 2-5 oligoadenylate synthetase-like 2 // 5 F|5 // 23962 /// ENSMUS	Oasl2	8.81E-05	-2.91964
NM_001025599 // Trim26 // tripartite motif-containing 26 // 17 B1|17 19.16 cM // 22670	Trim26	0.000142242	-2.91878
NM_027314 // March5 // membrane-associated ring finger (C3HC4) 5 // 19 C2|19 // 69104 /	Mar-05	4.17E-05	-2.91362
NM_021430 // Rilpl1 // Rab interacting lysosomal protein-like 1 // 5|5 F // 75695 /// X	Rilpl1	6.66E-07	-2.90529
ENSMUST00000158447 // Gm24500 // predicted gene, 24500 // --- // ---	Gm24500	0.00153043	-2.90352
NM_001290707 // Pde10a // phosphodiesterase 10A // 17 A1|17 // 23984 /// NM_011866 // P	Pde10a	0.000333274	-2.89956
ENSMUST00000030025 // Nr4a3 // nuclear receptor subfamily 4, group A, member 3 // 4|4 B	Nr4a3	0.000760406	-2.89816
NM_008418 // Kcna3 // potassium voltage-gated channel, shaker-related subfamily, member	Kcna3	0.000113443	-2.89687
NM_001198560 // H2-Q7 // histocompatibility 2, Q region locus 7 // 17 B1|17 18.67 cM //	H2-Q7	8.23E-05	-2.89627
NM_023141 // Tor3a // torsin family 3, member A // 1 H1|1 // 30935 /// ENSMUST000000796	Tor3a	5.71E-05	-2.89584
NM_133816 // Sh3bp4 // SH3-domain binding protein 4 // 1 D|1 // 98402 /// ENSMUST000000	Sh3bp4	2.29E-05	-2.89409
---		0.00189062	-2.88899
---		0.00343492	-2.88756
NM_001033245 // Hk3 // hexokinase 3 // 13 B1|13 // 212032 /// NM_001206390 // Hk3 // he	Hk3	5.21E-08	-2.88567

NM_001164062 // Stat5a // signal transducer and activator of transcription 5A // 11 D|1	Stat5a	4.27E-05	-2.88342
ENSMUST00000080694 // Gm5407 // predicted gene 5407 // --- // ---	Gm5407	0.0059683	-2.88233
NM_011930 // Clcn7 // chloride channel 7 // 17 A3.3|17 12.53 cM // 26373 /// ENSMUST000	Clcn7	9.23E-06	-2.88165
ENSMUST00000111360 // LOC100041057 // nuclear body protein SP140-like // 1|1 // 1000410	LOC100041057	0.00559857	-2.87914
NM_008655 // Gadd45b // growth arrest and DNA-damage-inducible 45 beta // 10 C1|10 39.7	Gadd45b	3.80E-05	-2.87576
NM_010231 // Fmo1 // flavin containing monooxygenase 1 // 1 H1|1 70.34 cM // 14261 ///	Fmo1	0.000151724	-2.87359
NM_010597 // Kcnab1 // potassium voltage-gated channel, shaker-related subfamily, beta	Kcnab1	1.42E-06	-2.87299
NM_001013371 // Dtx3l // deltex 3-like (Drosophila) // 16 B3|16 // 209200 /// ENSMUST00	Dtx3l	4.10E-06	-2.87272
NM_021604 // Agrn // agrin // 4 E2|4 88.55 cM // 11603 /// XM_006538496 // Agrn // agri	Agrn	1.97E-06	-2.87231
NM_178695 // Prrg4 // proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane) // 2	Prrg4	3.73E-05	-2.87075
NM_008466 // Kpna3 // karyopherin (importin) alpha 3 // 14 D1|14 // 16648 /// ENSMUST00	Kpna3	0.000175535	-2.85786
---		1.01E-05	-2.85751
NM_023044 // Slc15a3 // solute carrier family 15, member 3 // 19|19 B // 65221 /// ENSM	Slc15a3	2.78E-06	-2.85205
NM_001013779 // Aim2 // absent in melanoma 2 // 1 H3|1 // 383619 /// XM_006496915 // Ai	Aim2	3.01E-07	-2.84831
---		0.000479892	-2.84108
ENSMUST00000109212 // Gm5431 // predicted gene 5431 // 11 B1.2|11 // 432555	Gm5431	0.000368291	-2.83857
NM_198007 // Ascc3 // activating signal cointegrator 1 complex subunit 3 // 10 B3|10 //	Ascc3	2.66E-05	-2.83653
NR_045750 // Gm16675 // predicted gene, 16675 // 8|8 26.42 cM // 100503498 /// ENSMUST0	Gm16675	4.57E-05	-2.83423
NM_011785 // Akt3 // thymoma viral proto-oncogene 3 // 1|1 H4-H6 // 23797 /// XM_006496	Akt3	2.69E-06	-2.83234
ENSMUST00000032961 // Nupr1 // nuclear protein transcription regulator 1 // 7 F4|7 // 5	Nupr1	1.69E-05	-2.82846
---		5.86E-06	-2.82689
---		1.30E-05	-2.82541
---		0.00393222	-2.82483
NM_001177369 // Nfkb2 // nuclear factor of kappa light polypeptide gene enhancer in B c	Nfkb2	0.000452869	-2.82182
NM_026438 // Ppa1 // pyrophosphatase (inorganic) 1 // 10 B4|10 32.25 cM // 67895 /// EN	Ppa1	6.60E-07	-2.82124
NM_010156 // Samd9l // sterile alpha motif domain containing 9-like // 6 A1-A2|6 1.76 c	Samd9l	7.06E-06	-2.8199
NM_001146308 // Dbnl // drebrin-like // 11 A1|11 3.87 cM // 13169 /// NM_001146309 // D	Dbnl	2.51E-06	-2.81451
ENSMUST00000086787 // Tcp10b // t-complex protein 10b // 17 A1|17 7.8 cM // 21462 /// E	Tcp10b	0.00179069	-2.81369
ENSMUST00000172979 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17	H2-Q5	0.00166037	-2.81236
NM_009914 // Ccr3 // chemokine (C-C motif) receptor 3 // 9 F|9 75.05 cM // 12771 /// EN	Ccr3	0.00153383	-2.81185
NM_001290475 // Tdrd7 // tudor domain containing 7 // 4 B1|4 // 100121 /// NM_146142 //	Tdrd7	3.96E-06	-2.81041
---		0.000906269	-2.8103
NM_001008700 // Il4ra // interleukin 4 receptor, alpha // 7 F3|7 68.94 cM // 16190 ///	Il4ra	5.57E-07	-2.79727
NM_001112705 // Tlk2 // tousled-like kinase 2 (Arabidopsis) // 11 E1|11 // 24086 /// NM	Tlk2	2.73E-06	-2.79344
---		0.00103173	-2.79247
NM_133819 // Ppp1r15b // protein phosphatase 1, regulatory (inhibitor) subunit 15b // 1	Ppp1r15b	8.80E-07	-2.79245
NM_001136082 // Timeless // timeless circadian clock 1 // 10 D3|10 76.49 cM // 21853 //	Timeless	5.38E-05	-2.78894
NM_009546 // Trim25 // tripartite motif-containing 25 // 11 C|11 // 217069 /// ENSMUST0	Trim25	9.81E-06	-2.78856
NM_001113569 // Stxbp1 // syntaxin binding protein 1 // 2 B|2 22.09 cM // 20910 /// NM_	Stxbp1	1.26E-05	-2.78785
NM_009776 // Serping1 // serine (or cysteine) peptidase inhibitor, clade G, member 1 //	Serping1	0.000591374	-2.78757
NM_023248 // Sbds // Shwachman-Bodian-Diamond syndrome homolog (human) // 5 G1.3|5 // 6	Sbds	3.05E-07	-2.78703
NM_001191008 // Sstr5 // somatostatin receptor 5 // 17 A3.3|17 12.62 cM // 20609 /// NM	Sstr5	0.00144817	-2.785
NM_001003950 // Rab3ip // RAB3A interacting protein // 10 D2|10 64.96 cM // 216363 ///	Rab3ip	6.74E-06	-2.78464
NM_001172117 // Hck // hemopoietic cell kinase // 2 H1|2 75.41 cM // 15162 /// NM_01040	Hck	0.000241876	-2.78393
ENSMUST00000073080 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063	Cycs	9.81E-05	-2.78055
NM_028810 // Rnd3 // Rho family GTPase 3 // 2 C1.1|2 // 74194 /// ENSMUST00000017288 //	Rnd3	3.20E-05	-2.77978
NM_001081223 // Rbbp8 // retinoblastoma binding protein 8 // 18 A1|18 // 225182 /// NM_	Rbbp8	0.000110373	-2.77921
NM_025821 // Carhsp1 // calcium regulated heat stable protein 1 // 16 A1|16 4.26 cM //	Carhsp1	3.45E-05	-2.77454
ENSMUST00000168554 // Gm5423 // predicted gene 5423 // --- // ---	Gm5423	0.000937776	-2.7709
---		0.000592109	-2.76584
NM_010171 // F3 // coagulation factor III // 3 G1|3 52.94 cM // 14066 /// ENSMUST000000	F3	0.00108515	-2.76493
NM_001201341 // Msi2 // musashi RNA-binding protein 2 // 11 C|11 // 76626 /// NM_054043	Msi2	3.71E-05	-2.76003
NM_010397 // H2-T22 // histocompatibility 2, T region locus 22 // 17 B1|17 18.87 cM //	H2-T22	0.000230093	-2.75415
NM_030694 // Ifitm2 // interferon induced transmembrane protein 2 // 7|7 F5 // 80876 //	Ifitm2	0.000156028	-2.75311
NM_001005846 // Mcoln2 // mucolipin 2 // 3 H2|3 // 68279 /// NM_026656 // Mcoln2 // muc	Mcoln2	3.03E-06	-2.74461
NM_007602 // Capn5 // calpain 5 // 7 E2|7 // 12337 /// XM_006507275 // Capn5 // calpain	Capn5	3.33E-07	-2.74307
NM_172839 // Ccnj // cyclin J // 19 C3|19 // 240665 /// ENSMUST00000025983 // Ccnj // c	Ccnj	4.94E-05	-2.74249
NM_001290822 // Pdpn // podoplanin // 4 E1|4 // 14726 /// NM_010329 // Pdpn // podoplan	Pdpn	6.31E-07	-2.73661
NM_008630 // Mt2 // metallothionein 2 // 8 C5|8 46.32 cM // 17750 /// ENSMUST0000003421	Mt2	0.00131595	-2.73021
NM_031373 // Ogfr // opioid growth factor receptor // 2 H4|2 // 72075 /// ENSMUST000000	Ogfr	8.33E-07	-2.7299
NM_001289926 // 2010111I01Rik // RIKEN cDNA 2010111I01 gene // 13 B3|13 // 72061 /// NR	2010111I01Rik	0.00117493	-2.72839
NM_001159407 // B3gnt5 // UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	B3gnt5	0.00279012	-2.72786
NM_001081029 // Tmem243 // transmembrane protein 243, mitochondrial // 5 A1|5 // 652925	Tmem243	1.29E-05	-2.72728
NM_001081162 // Slc4a11 // solute carrier family 4, sodium bicarbonate transporter-like	Slc4a11	0.000312502	-2.72345
NM_009982 // Ctsc // cathepsin C // 7|7 D3-E1.1 // 13032 /// ENSMUST00000032779 // Ctsc	Ctsc	0.000249848	-2.7162
NM_172282 // Tmco3 // transmembrane and coiled-coil domains 3 // 8 A1.1|8 // 234076 ///	Tmco3	1.63E-06	-2.71428
NM_001286226 // Cacnb3 // calcium channel, voltage-dependent, beta 3 subunit // 15 F1|1	Cacnb3	8.10E-05	-2.71221
ENSMUST00000129498 // Mrpl27 // mitochondrial ribosomal protein L27 // 11 D|11 58.9 cM	Mrpl27	0.00603813	-2.70878
NM_008884 // Pml // promyelocytic leukemia // 9 B|9 31.63 cM // 18854 /// NM_178087 //	Pml	1.55E-05	-2.70019
NM_028808 // P2ry13 // purinergic receptor P2Y, G-protein coupled 13 // 3 D|3 // 74191	P2ry13	4.84E-06	-2.69992
ENSMUST00000124513 // Gm15247 // predicted gene 15247 // --- // --- /// AK019053 // Gm1	Gm15247	0.000130137	-2.69064
NM_207160 // Olfr519 // olfactory receptor 519 // 7 E3|7 // 277935 /// ENSMUST000000847	Olfr519	0.000383568	-2.68993
NM_013640 // Psmb10 // proteasome (prosome, macropain) subunit, beta type 10 // 8 D3|8	Psmb10	0.000272	-2.68836
NM_001163136 // Macc1 // metastasis associated in colon cancer 1 // 12 F2|12 // 238455	Macc1	0.000216823	-2.68798
NM_013885 // Clic4 // chloride intracellular channel 4 (mitochondrial) // 4 D3|4 // 298	Clic4	0.000164696	-2.68737
NM_001168684 // Tmcc3 // transmembrane and coiled coil domains 3 // 10 C2|10 // 319880	Tmcc3	0.000244854	-2.68398
XM_986941 // Ms4a4a // membrane-spanning 4-domains, subfamily A, member 4A // 19 A|19 /	Ms4a4a	3.55E-05	-2.6816
NM_008990 // Pvrl2 // poliovirus receptor-related 2 // 7 A3|7 9.94 cM // 19294 /// ENSM	Pvrl2	3.43E-05	-2.67659
NM_031181 // Siglece // sialic acid binding Ig-like lectin E // 7 B2|7 // 83382 /// XM_	Siglece	0.000741507	-2.67122
NM_001205313 // Stat1 // signal transducer and activator of transcription 1 // 1 C1.1|1	Stat1	0.000413468	-2.66534
NM_197944 // Hsh2d // hematopoietic SH2 domain containing // 8 B3.3|8 // 209488 /// ENS	Hsh2d	0.000138819	-2.66396
NM_011890 // Sgcb // sarcoglycan, beta (dystrophin-associated glycoprotein) // 5 C3.3|5	Sgcb	4.91E-08	-2.6633
NM_018866 // Cxcl13 // chemokine (C-X-C motif) ligand 13 // 5 E3|5 // 55985 /// ENSMUST	Cxcl13	0.0023243	-2.66117
NM_001204983 // Cep85l // centrosomal protein 85-like // 10|10 // 100038725 /// XM_0065	Cep85l	0.000177066	-2.66046
NM_207636 // Fndc3a // fibronectin type III domain containing 3A // 14 D2|14 37.62 cM /	Fndc3a	4.31E-06	-2.66011
NM_019807 // Acpp // acid phosphatase, prostate // 9 F1|9 // 56318 /// NM_207668 // Acp	Acpp	5.99E-05	-2.65937
---		0.00430703	-2.65557
NM_013880 // Plcl2 // phospholipase C-like 2 // 17 C|17 // 224860 /// XM_006524150 // P	Plcl2	8.39E-06	-2.65374
NM_172593 // Mier3 // mesoderm induction early response 1, family member 3 // 13 D2.2|1	Mier3	4.93E-07	-2.64631

NM_007544 // Bid // BH3 interacting domain death agonist // 6 F1|6 57.02 cM // 12122 //	Bid	4.73E-05	-2.64376
NM_148927 // Plekha4 // pleckstrin homology domain containing, family A (phosphoinositi	Plekha4	0.000155163	-2.6432
NM_001024624 // Cdkl5 // cyclin-dependent kinase-like 5 // X F4|X 73.95 cM // 382253 //	Cdkl5	9.14E-05	-2.63964
NM_001167991 // Hook2 // hook homolog 2 (Drosophila) // 8 C3|8 // 170833 /// NM_133255	Hook2	0.000535584	-2.63804
NM_001253817 // Tmem184b // transmembrane protein 184b // 15 E1|15 // 223693 /// NM_001	Tmem184b	1.16E-06	-2.63139
NM_001161774 // St3gal3 // ST3 beta-galactoside alpha-2,3-sialyltransferase 3 // 4|4 D1	St3gal3	5.36E-05	-2.6292
NM_172668 // Lrp4 // low density lipoprotein receptor-related protein 4 // 2 E1|2 50.63	Lrp4	0.000188915	-2.62762
NM_199195 // Bckdhb // branched chain ketoacid dehydrogenase E1, beta polypeptide // 9	Bckdhb	5.94E-06	-2.62493
NM_133888 // Smpdl3b // sphingomyelin phosphodiesterase, acid-like 3B // 4 D2.3|4 // 10	Smpdl3b	0.000453956	-2.62294
ENSMUST00000123363 // Gm16014 // predicted gene 16014 // --- // ---	Gm16014	0.000530995	-2.62098
NR_037271 // Mir3088 // microRNA 3088 // 2|2 19.38 cM // 100526498 /// ENSMUST000001750	Mir3088	0.00410039	-2.61785
ENSMUST00000172796 // Gm20496 // predicted gene 20496 // --- // --- /// ENSMUST00000173	Gm20496	0.0035479	-2.61755
NM_001033196 // Znfx1 // zinc finger, NFX1-type containing 1 // 2 H3|2 // 98999 /// ENS	Znfx1	1.90E-05	-2.61267
NM_054041 // Antxr1 // anthrax toxin receptor 1 // 6 D1|6 // 69538 /// XM_006506564 //	Antxr1	3.06E-07	-2.61059
NM_026115 // Hat1 // histone aminotransferase 1 // 2 C2|2 // 107435 /// ENSMUST00000028	Hat1	7.68E-06	-2.60917
NM_011756 // Zfp36 // zinc finger protein 36 // 7 A3|7 16.72 cM // 22695 /// ENSMUST000	Zfp36	4.21E-05	-2.6044
NM_001145924 // Msantd3 // Myb/SANT-like DNA-binding domain containing 3 // 4|4 B2 // 6	Msantd3	0.00128495	-2.60401
---		0.000680801	-2.60022
ENSMUST00000157375 // Gm25493 // predicted gene, 25493 // --- // ---	Gm25493	0.00197975	-2.59655
NM_019636 // Tbc1d1 // TBC1 domain family, member 1 // 5 C3.1|5 // 57915 /// ENSMUST000	Tbc1d1	3.35E-05	-2.59412
NM_007791 // Csrp1 // cysteine and glycine-rich protein 1 // 1 E4|1 // 13007 /// ENSMUS	Csrp1	2.03E-06	-2.59185
NM_001038587 // Adar // adenosine deaminase, RNA-specific // 3|3 F2 // 56417 /// NM_001	Adar	3.10E-06	-2.58922
NM_008385 // Inpp5b // inositol polyphosphate-5-phosphatase B // 4 D2|4 57.89 cM // 163	Inpp5b	1.60E-07	-2.58506
NM_177368 // Tmtc2 // transmembrane and tetratricopeptide repeat containing 2 // 10 D1|	Tmtc2	0.000262898	-2.58497
---		0.00332048	-2.58291
NM_008748 // Dusp8 // dual specificity phosphatase 8 // 7 F5|7 87.59 cM // 18218 /// EN	Dusp8	0.00129386	-2.58105
NM_013529 // Gfpt2 // glutamine fructose-6-phosphate transaminase 2 // 11 B1.2|11 29.9	Gfpt2	0.000378559	-2.57876
---		0.000157823	-2.57859
NM_027890 // Susd2 // sushi domain containing 2 // 10|10 B5.3 // 71733 /// ENSMUST00000	Susd2	0.000129425	-2.57846
NM_172785 // Zc3h12d // zinc finger CCCH type containing 12D // 10 A1|10 // 237256 ///	Zc3h12d	0.000329003	-2.57572
NM_020498 // Ly6i // lymphocyte antigen 6 complex, locus I // 15 D3|15 // 57248 /// ENS	Ly6i	0.00118703	-2.57413
XM_006514332 // Misp // mitotic spindle positioning // 10 C1|10 // 78906 /// XM_0065143	Misp	0.00097045	-2.57303
NM_007892 // E2f5 // E2F transcription factor 5 // 3 A1|3 // 13559 /// XM_006530051 //	E2f5	0.000124627	-2.56904
NM_177910 // Gmppb // GDP-mannose pyrophosphorylase B // 9 F2|9 // 331026 /// ENSMUST00	Gmppb	6.93E-05	-2.56749
NM_001160181 // Tor1aip2 // torsin A interacting protein 2 // 1 G3|1 // 240832 /// NM_0	Tor1aip2	2.32E-05	-2.56739
NM_011957 // Creb3l1 // cAMP responsive element binding protein 3-like 1 // 2 E1|2 // 2	Creb3l1	0.000360634	-2.56304
---		0.000570072	-2.56283
NM_145619 // Parp3 // poly (ADP-ribose) polymerase family, member 3 // 9 F1|9 // 235587	Parp3	5.41E-06	-2.55938
NM_023440 // Tmem86b // transmembrane protein 86B // 7 A1|7 // 68255 /// ENSMUST0000005	Tmem86b	0.0033071	-2.55835
NM_001039537 // Lif // leukemia inhibitory factor // 11 A1-A2|11 2.94 cM // 16878 /// E	Lif	0.000137818	-2.55526
---		2.51E-06	-2.55492
AK052181 // Gm9883 // predicted gene 9883 // 19 C1|19 // 791409	Gm9883	8.02E-05	-2.5535
AK052181 // Gm9883 // predicted gene 9883 // 19 C1|19 // 791409	Gm9883	8.02E-05	-2.5535
NM_001081009 // Parp8 // poly (ADP-ribose) polymerase family, member 8 // 13 D2.3|13 65	Parp8	4.65E-06	-2.55263
---		0.00442567	-2.54895
NM_001035532 // Akap2 // A kinase (PRKA) anchor protein 2 // 4 B3|4 // 11641 /// NM_001	Akap2	2.40E-05	-2.54216
NM_178098 // 4930486L24Rik // RIKEN cDNA 4930486L24 gene // 13 B2|13 // 214639 /// ENSM	4930486L24Rik	0.00125454	-2.53976
ENSMUST00000083829 // Gm23847 // predicted gene, 23847 // --- // ---	Gm23847	0.0053704	-2.53823
NM_028019 // Rnf135 // ring finger protein 135 // 11 B5|11 47.59 cM // 71956 /// ENSMUS	Rnf135	4.50E-05	-2.53795
NM_010169 // F2r // coagulation factor II (thrombin) receptor // 13 D1|13 50.21 cM // 1	F2r	0.000444757	-2.53655
---		0.00514864	-2.53618
NM_001159393 // Irf1 // interferon regulatory factor 1 // 11 B1.3|11 32.0 cM // 16362 /	Irf1	0.00192183	-2.53251
---		0.00676113	-2.53173
NM_182806 // Gpr18 // G protein-coupled receptor 18 // 14 E5|14 65.86 cM // 110168 ///	Gpr18	0.00403693	-2.53052
NM_181732 // Aida // axin interactor, dorsalization associated // 1|1 // 108909 /// ENS	Aida	2.67E-06	-2.52614
NM_177855 // Med12l // mediator complex subunit 12-like // 3 D|3 // 329650 /// ENSMUST0	Med12l	0.00151203	-2.52248
NM_026960 // Gsdmd // gasdermin D // 15|15 D3-E1 // 69146 /// XM_006521343 // Gsdmd //	Gsdmd	8.52E-06	-2.52115
ENSMUST00000175017 // Gm25026 // predicted gene, 25026 // --- // ---	Gm25026	0.00199338	-2.51863
NM_009808 // Casp12 // caspase 12 // 9 A1|9 2.46 cM // 12364 /// ENSMUST00000027009 //	Casp12	0.000847428	-2.51778
---		0.00154045	-2.51761
ENSMUST00000032815 // Nfkbib // nuclear factor of kappa light polypeptide gene enhancer	Nfkbib	0.000240455	-2.51652
ENSMUST00000163802 // Gm17139 // predicted gene 17139 // --- // ---	Gm17139	0.00617342	-2.51333
ENSMUST00000160445 // Gm16549 // predicted gene 16549 // --- // --- /// AK007062 // Fnd	Gm16549	0.000116497	-2.51224
NM_008927 // Map2k1 // mitogen-activated protein kinase kinase 1 // 9 C|9 34.55 cM // 2	Map2k1	2.92E-07	-2.51143
NM_001164314 // Wars // tryptophanyl-tRNA synthetase // 12|12 F2 // 22375 /// NM_001164	Wars	2.76E-06	-2.50916
NM_001289704 // Cflar // CASP8 and FADD-like apoptosis regulator // 1 C1.3|1 29.16 cM /	Cflar	0.00142119	-2.50854
NM_001099217 // Ly6c2 // lymphocyte antigen 6 complex, locus C2 // 15 D3|15 // 10004154	Ly6c2	0.00129226	-2.50822
NM_028341 // Ttc39c // tetratricopeptide repeat domain 39C // 18|18 A2 // 72747 /// XM_	Ttc39c	5.96E-06	-2.5068
NM_175401 // Fbxw17 // F-box and WD-40 domain protein 17 // 13 A5|13 // 109082 /// XM_0	Fbxw17	1.16E-07	-2.50592
NR_045932 // Slfn5os // schlafen 5, opposite strand // 11 C|11 // 76392 /// ENSMUST0000	Slfn5os	5.37E-05	-2.50578
ENSMUST00000067924 // Lrrc8c // leucine rich repeat containing 8 family, member C // 5	Lrrc8c	2.51E-05	-2.50246
ENSMUST00000031264 // Plac8 // placenta-specific 8 // 5 E3|5 48.49 cM // 231507 /// ENS	Plac8	0.000376718	-2.4996
---		0.00651262	-2.4982
NM_009189 // Six1 // sine oculis-related homeobox 1 // 12 C3|12 30.34 cM // 20471 /// E	Six1	0.000483679	-2.49804
NM_011580 // Thbs1 // thrombospondin 1 // 2 F1-F3|2 59.34 cM // 21825 /// ENSMUST000000	Thbs1	5.76E-06	-2.49643
ENSMUST00000083384 // Gm24099 // predicted gene, 24099 // --- // ---	Gm24099	0.000256886	-2.49416
NM_001159301 // Lgals9 // lectin, galactose binding, soluble 9 // 11 B5|11 // 16859 ///	Lgals9	0.000260481	-2.49061
NM_011521 // Sdc4 // syndecan 4 // 2 H3|2 85.16 cM // 20971 /// ENSMUST00000017153 // S	Sdc4	0.00196069	-2.4905
AK079938 // BE692007 // expressed sequence BE692007 // 19|19 8.44 cM // 100504727 /// X	BE692007	0.00391186	-2.48947
---		9.26E-05	-2.48864
NM_144905 // 6330416G13Rik // RIKEN cDNA 6330416G13 gene // 4 C1|4 // 230279 /// XM_006	6330416G13Rik	4.18E-05	-2.48765
NM_001110254 // Zfp945 // zinc finger protein 945 // 17 A3.3|17 // 240041 /// NM_177358	Zfp945	0.000156425	-2.48507
ENSMUST00000178911 // Gm8324 // predicted gene 8324 // --- // ---	Gm8324	0.00209703	-2.48312
---		0.00214769	-2.48167
NM_172647 // F11r // F11 receptor // 1 H2|1 79.43 cM // 16456 /// ENSMUST00000043839 //	F11r	0.000303267	-2.47178
NM_001048146 // Azi2 // 5-azacytidine induced gene 2 // 9 F3|9 // 27215 /// NM_00128650	Azi2	1.00E-08	-2.46941
ENSMUST00000170390 // Irf1 // interferon regulatory factor 1 // 11 B1.3|11 32.0 cM // 1	Irf1	0.00226821	-2.46905
NM_001289915 // Cd83 // CD83 antigen // 13 A4-5|13 21.6 cM // 12522 /// NM_009856 // Cd	Cd83	2.58E-05	-2.46836
XM_006510634 // Ubash3b // ubiquitin associated and SH3 domain containing, B // 9 A5.1|	Ubash3b	6.35E-05	-2.45831

NM_028381 // Ccdc94 // coiled-coil domain containing 94 // 17 D|17 // 72886 /// ENSMUST	Ccdc94	8.45E-06	-2.45694
NM_010742 // Ly6d // lymphocyte antigen 6 complex, locus D // 15 D3|15 34.27 cM // 1706	Ly6d	0.000394887	-2.45541
ENSMUST00000034522 // Clmp // CXADR-like membrane protein // 9 A5.1|9 // 71566 /// NM_1	Clmp	7.20E-12	-2.45509
NM_026001 // Rnaseh2b // ribonuclease H2, subunit B // 14 D1|14 // 67153 /// ENSMUST000	Rnaseh2b	0.000332382	-2.45507
NM_028451 // Larp1 // La ribonucleoprotein domain family, member 1 // 11|11 B2 // 73158	Larp1	3.70E-05	-2.45499
NR_051981 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 15	H2-Q5	0.000981177	-2.45331
ENSMUST00000112618 // Gpd2 // glycerol phosphate dehydrogenase 2, mitochondrial // 2 C1	Gpd2	0.000287649	-2.45172
NM_001163489 // Sema4a // sema domain, immunoglobulin domain (Ig), transmembrane domain	Sema4a	4.07E-08	-2.45132
NR_037982 // 9330159M07Rik // RIKEN cDNA 9330159M07 gene // 9|9 // 319673	9330159M07Ri	0.00162507	-2.45025
---		0.000914561	-2.4501
ENSMUST00000103922 // Gm22427 // predicted gene, 22427 // --- // ---	Gm22427	2.41E-05	-2.44595
NM_001145799 // Ctla2a // cytotoxic T lymphocyte-associated protein 2 alpha // 13 B2|13	Ctla2a	0.00568309	-2.44321
XR_106025 // LOC100503338 // uncharacterized LOC100503338 // --- // 100503338 /// ENSMU	LOC100503338	0.000330646	-2.44293
NM_001163645 // Osbpl3 // oxysterol binding protein-like 3 // 6|6 B3 // 71720 /// NM_02	Osbpl3	5.41E-05	-2.44221
NM_011347 // Selp // selectin, platelet // 1 H2.2|1 71.42 cM // 20344 /// ENSMUST000001	Selp	0.00496961	-2.44217
ENSMUST00000175407 // Gm23375 // predicted gene, 23375 // --- // --- /// ENSMUST0000009	Gm23375	8.35E-05	-2.44033
ENSMUST00000141741 // Gm16933 // predicted gene, 16933 // --- // --- /// AK041498 // Pl	Gm16933	0.000112409	-2.43898
NR_001584 // Speer8-ps1 // spermatogenesis associated glutamate (E)-rich protein 8, pse	Speer8-ps1	0.00500124	-2.43793
NM_018782 // Calcrl // calcitonin receptor-like // 2 D|2 // 54598 /// ENSMUST0000007426	Calcrl	1.95E-05	-2.43711
NM_011809 // Ets2 // E26 avian leukemia oncogene 2, 3 domain // 16 C3-qter|16 56.64 cM	Ets2	5.96E-06	-2.43676
ENSMUST00000083239 // Gm22127 // predicted gene, 22127 // --- // ---	Gm22127	0.00427919	-2.42909
NM_011817 // Gadd45g // growth arrest and DNA-damage-inducible 45 gamma // 13|13 A5-B /	Gadd45g	3.81E-06	-2.42858
NM_009621 // Adamts1 // a disintegrin-like and metallopeptidase (reprolysin type) with	Adamts1	0.00164919	-2.42763
NM_021788 // Sap30 // sin3 associated polypeptide // 8 B2|8 29.85 cM // 60406 /// ENSMU	Sap30	1.23E-06	-2.42748
NM_183201 // Slfn5 // schlafen 5 // 11 C|11 // 327978 /// XR_388481 // Slfn5 // schlafe	Slfn5	0.000146777	-2.42458
ENSMUST00000049281 // Fam53c // family with sequence similarity 53, member C // 18 B1|1	Fam53c	0.000295537	-2.42399
NM_001285959 // Lyrm1 // LYR motif containing 1 // 7 F2|7 // 73919 /// NM_001285960 //	Lyrm1	0.00450329	-2.42181
NM_009878 // Cdkn2d // cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) // 9 A	Cdkn2d	8.86E-05	-2.4217
NM_026827 // Tmem219 // transmembrane protein 219 // 7|7 F4 // 68742 /// NM_028389 // T	Tmem219	5.21E-05	-2.42085
NM_013825 // Ly75 // lymphocyte antigen 75 // 2 C1.1|2 // 17076 /// ENSMUST00000028362	Ly75	0.000143763	-2.42025
NM_001146176 // Max // Max protein // 12 D1-D3|12 33.78 cM // 17187 /// NM_008558 // Ma	Max	2.64E-07	-2.41925
NM_001014996 // Cenpj // centromere protein J // 14 C3|14 // 219103 /// ENSMUST00000065	Cenpj	0.000106316	-2.41439
NM_028595 // Ms4a6c // membrane-spanning 4-domains, subfamily A, member 6C // 19 A|19 /	Ms4a6c	0.000115983	-2.413
---		0.00109035	-2.4127
---		0.000154202	-2.4125
NM_008146 // Golga3 // golgi autoantigen, golgin subfamily a, 3 // 5 F|5 53.36 cM // 26	Golga3	9.39E-05	-2.41198
NM_001141981 // Rbm43 // RNA binding motif protein 43 // 2|2 C1 // 71684 /// NM_0011419	Rbm43	1.29E-06	-2.41014
NM_001038641 // Slx4ip // SLX4 interacting protein // 2|2 G1 // 74243 /// NM_028201 //	Slx4ip	0.00500833	-2.40446
NM_013642 // Dusp1 // dual specificity phosphatase 1 // 17 A2-C|17 13.28 cM // 19252 //	Dusp1	5.32E-07	-2.40218
NM_172815 // Rspo2 // R-spondin 2 homolog (Xenopus laevis) // 15 B3.1-B3.2|15 16.73 cM	Rspo2	5.13E-05	-2.40182
NM_001254946 // BC035044 // cDNA sequence BC035044 // 6 F3|6 // 232406 /// ENSMUST00000	BC035044	0.000135768	-2.40145
NM_153074 // Lrrc25 // leucine rich repeat containing 25 // 8 B3.3|8 // 211228 /// ENSM	Lrrc25	0.000221657	-2.40136
---		0.00506057	-2.3998
---		0.00506057	-2.3998
NM_001113530 // Csf1 // colony stimulating factor 1 (macrophage) // 3 F3|3 46.83 cM //	Csf1	4.50E-07	-2.39582
NM_030017 // Rdh12 // retinol dehydrogenase 12 // 12|12 D2 // 77974 /// XM_006516372 //	Rdh12	6.73E-05	-2.39497
NR_030490 // Mir709 // microRNA 709 // 8|8 // 735271 /// ENSMUST00000102190 // Mir709 /	Mir709	0.00111321	-2.39326
NM_015766 // Ebi3 // Epstein-Barr virus induced gene 3 // 17 D|17 29.08 cM // 50498 ///	Ebi3	0.000103225	-2.39155
NM_001161770 // Lmo4 // LIM domain only 4 // 3 H2|3 68.61 cM // 16911 /// ENSMUST000001	Lmo4	3.75E-05	-2.39121
---		0.00131556	-2.39052
NM_019471 // Mmp10 // matrix metallopeptidase 10 // 9 A1|9 // 17384 /// ENSMUST00000034	Mmp10	0.00176886	-2.39029
NM_029362 // Chmp4b // charged multivesicular body protein 4B // 2|2 H2 // 75608 /// EN	Chmp4b	3.40E-08	-2.38818
NM_001045514 // Akna // AT-hook transcription factor // 4 C1|4 // 100182 /// XM_0065375	Akna	0.00154755	-2.38814
ENSMUST00000055018 // Lpar1 // lysophosphatidic acid receptor 1 // 4 B3|4 32.2 cM // 14	Lpar1	0.000159378	-2.38708
---		0.00041386	-2.38616
ENSMUST00000025684 // Ehd1 // EH-domain containing 1 // 19 A|19 4.4 cM // 13660 /// AK0	Ehd1	0.00502344	-2.38059
ENSMUST00000113438 // Adamts9 // a disintegrin-like and metallopeptidase (reprolysin ty	Adamts9	0.00245839	-2.37817
ENSMUST00000091905 // Gm4950 // predicted pseudogene 4950 // --- // ---	Gm4950	0.00360783	-2.37769
ENSMUST00000157685 // Gm26183 // predicted gene, 26183 // --- // ---	Gm26183	0.00387953	-2.37758
NM_025697 // Spryd7 // SPRY domain containing 7 // 14 D1|14 // 66674 /// XM_006519394 /	Spryd7	3.33E-06	-2.37345
NM_178065 // Arel1 // apoptosis resistant E3 ubiquitin protein ligase 1 // 12 D2|12 //	Arel1	4.63E-06	-2.37271
NM_018830 // Asah2 // N-acylsphingosine amidohydrolase 2 // 19|19 C3 // 54447 /// ENSMU	Asah2	0.000473136	-2.37084
NR_004446 // H2-K2 // histocompatibility 2, K region locus 2 // 17 B1|17 17.98 cM // 63	H2-K2	0.00655311	-2.36984
NM_010904 // Nefh // neurofilament, heavy polypeptide // 11 A1-A5|11 3.12 cM // 380684	Nefh	0.00645363	-2.36872
NM_001286040 // Anks1 // ankyrin repeat and SAM domain containing 1 // 17 A3.3|17 // 22	Anks1	1.85E-05	-2.3683
NM_173386 // Mb21d1 // Mab-21 domain containing 1 // 9 E1|9 // 214763 /// ENSMUST000000	Mb21d1	0.00170559	-2.36817
NM_009969 // Csf2 // colony stimulating factor 2 (granulocyte-macrophage) // 11 B1.3|11	Csf2	0.000541016	-2.36396
XR_379082 // LOC102639683 // uncharacterized LOC102639683 // --- // 102639683 /// ENSMU	LOC102639683	0.0041535	-2.36247
NM_146168 // Vopp1 // vesicular, overexpressed in cancer, prosurvival protein 1 // 6 B3	Vopp1	0.000178582	-2.36242
NM_025730 // Lrrk2 // leucine-rich repeat kinase 2 // 15|15 F1 // 66725 /// XM_00652127	Lrrk2	7.71E-05	-2.36153
ENSMUST00000077472 // Chst15 // carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulf	Chst15	4.41E-05	-2.36094
NM_019835 // B4galt5 // UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide	B4galt5	1.77E-06	-2.36076
NM_001005740 // Phactr1 // phosphatase and actin regulator 1 // 13 A4|13 // 218194 ///	Phactr1	0.000336596	-2.35827
ENSMUST00000074761 // Gm10134 // predicted gene 10134 // --- // --- /// AK136568 // Gm1	Gm10134	0.002436	-2.35481
ENSMUST00000181718 // Gm26750 // predicted gene, 26750 // --- // ---	Gm26750	0.000511348	-2.35454
XR_388923 // LOC102635154 // uncharacterized LOC102635154 // --- // 102635154 /// XR_38	LOC102635154	0.00108419	-2.35308
NM_001005510 // Syne2 // spectrin repeat containing, nuclear envelope 2 // 12 C3|12 33.	Syne2	0.000318676	-2.35178
NM_001163686 // Dok5 // docking protein 5 // 2 H3|2 92.26 cM // 76829 /// NM_029761 //	Dok5	0.00143846	-2.34849
XM_006538833 // Tnfrsf14 // tumor necrosis factor receptor superfamily, member 14 (herp	Tnfrsf14	3.05E-05	-2.34782
NM_007961 // Etv6 // ets variant 6 // 6 G2|6 64.58 cM // 14011 /// XM_006505514 // Etv6	Etv6	1.23E-05	-2.34734
NM_178592 // Abhd16a // abhydrolase domain containing 16A // 17 B1|17 18.59 cM // 19374	Abhd16a	1.44E-06	-2.34639
NM_001162909 // Spaca6 // sperm acrosome associated 6 // 17 A3.2|17 // 75202 /// ENSMUS	Spaca6	0.00097541	-2.34421
NM_001288586 // Mdm2 // transformed mouse 3T3 cell double minute 2 // 10 C1-C3|10 66.32	Mdm2	3.51E-06	-2.34001
NM_207209 // Sec24b // Sec24 related gene family, member B (S. cerevisiae) // 3 G3|3 //	Sec24b	3.27E-05	-2.33746
NM_001080818 // Cdc14a // CDC14 cell division cycle 14A // 3 G1|3 // 229776 /// NM_0011	Cdc14a	0.000501833	-2.33691
NM_021547 // Stard3 // START domain containing 3 // 11 D|11 // 59045 /// XM_006533897 /	Stard3	3.00E-06	-2.33662
NM_001110209 // Lnp // limb and neural patterns // 2 C3|2 // 69605 /// NM_027133 // Lnp	Lnp	3.16E-07	-2.33299
---		0.000636592	-2.33132
NM_028627 // Psd // pleckstrin and Sec7 domain containing // 19 C3|19 38.8 cM // 73728	Psd	0.00150176	-2.33058

---		0.00105417	-2.32838
NM_018776 // Crlf3 // cytokine receptor-like factor 3 // 11 B5|11 47.43 cM // 54394 ///	Crlf3	0.000301467	-2.32813
ENSMUST00000151282 // Gm11706 // predicted gene 11706 // --- // ---	Gm11706	0.000672326	-2.32405
---		3.88E-05	-2.32034
NM_030743 // Rnf114 // ring finger protein 114 // 2 H3|2 // 81018 /// XM_006500439 // R	Rnf114	3.55E-06	-2.31856
NM_001113326 // Msr1 // macrophage scavenger receptor 1 // 8 A4|8 23.89 cM // 20288 ///	Msr1	3.60E-06	-2.31852
ENSMUST00000079684 // Gm8394 // predicted gene 8394 // --- // ---	Gm8394	1.12E-06	-2.31798
NM_001008549 // Zfp658 // zinc finger protein 658 // 7 B4|7 // 210104 /// ENSMUST000001	Zfp658	0.0021967	-2.31791
---		0.00225795	-2.31784
NM_001033362 // Gm614 // predicted gene 614 // X D|X // 245536 /// ENSMUST00000101358 /	Gm614	8.90E-05	-2.31763
NM_007553 // Bmp2 // bone morphogenetic protein 2 // 2 F2|2 65.21 cM // 12156 /// ENSMU	Bmp2	0.000119543	-2.31558
NM_146122 // Dennd1a // DENN/MADD domain containing 1A // 2 B|2 // 227801 /// ENSMUST00	Dennd1a	8.77E-05	-2.3146
NM_010724 // Psmb8 // proteasome (prosome, macropain) subunit, beta type 8 (large multi	Psmb8	1.39E-06	-2.31414
NM_010361 // Gstt2 // glutathione S-transferase, theta 2 // 10 B5-C1|10 38.58 cM // 148	Gstt2	0.00145952	-2.31344
NM_001081105 // Rhoh // ras homolog gene family, member H // 5|5 D // 74734 /// ENSMUST	Rhoh	0.000604671	-2.31303
NM_029077 // Trim14 // tripartite motif-containing 14 // 4|4 B2 // 74735 /// ENSMUST000	Trim14	8.68E-06	-2.30868
NM_026386 // Snx2 // sorting nexin 2 // 18 D1|18 // 67804 /// ENSMUST00000037850 // Snx	Snx2	1.11E-05	-2.30859
---		0.00616137	-2.30841
XM_006499876 // Shf // Src homology 2 domain containing F // 2 E5|2 // 435684 /// NM_00	Shf	0.00029808	-2.30765
NM_001142952 // Fam46c // family with sequence similarity 46, member C // 3 F2.2|3 // 7	Fam46c	0.000145702	-2.30754
NM_008211 // H3f3b // H3 histone, family 3B // 11 E2|11 // 15081 /// XM_006532248 // H3	H3f3b	2.15E-05	-2.30571
NM_010945 // Nsmaf // neutral sphingomyelinase (N-SMase) activation associated factor /	Nsmaf	4.95E-06	-2.30441
NM_021397 // Zbtb32 // zinc finger and BTB domain containing 32 // 7 B2-B3|7 // 58206 /	Zbtb32	0.000771819	-2.30333
XR_378383 // LOC102638993 // uncharacterized LOC102638993 // --- // 102638993 /// XR_37	LOC102638993	0.00526386	-2.30311
NM_001201460 // H2-Q9 // histocompatibility 2, Q region locus 9 // 17|17 // 110558 ///	H2-Q9	3.76E-05	-2.30262
NM_001159633 // Slc44a1 // solute carrier family 44, member 1 // 4 B2|4 // 100434 /// N	Slc44a1	3.20E-06	-2.30246
NM_011074 // Cdk14 // cyclin-dependent kinase 14 // 5 A1|5 2.61 cM // 18647 /// XM_0065	Cdk14	0.000429088	-2.30197
NM_010851 // Myd88 // myeloid differentiation primary response gene 88 // 9 F3|9 71.33	Myd88	0.00010043	-2.30181
NM_001024716 // Triobp // TRIO and F-actin binding protein // 15 E1|15 37.7 cM // 11025	Triobp	2.12E-05	-2.30156
NR_003363 // Gm6548 // eukaryotic translation elongation factor 1 alpha 1 pseudogene //	Gm6548	2.85E-05	-2.30111
---		0.000963336	-2.30072
NM_172831 // E230025N22Rik // Riken cDNA E230025N22 gene // 18 B2|18 // 240216 /// XM_0	E230025N22Rik	0.00588126	-2.29493
NM_007808 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063 /// ENSMUST000	Cycs	9.31E-05	-2.28999
NM_001008233 // Plekhn1 // pleckstrin homology domain containing, family N member 1 //	Plekhn1	0.000130854	-2.28824
ENSMUST00000174699 // H2-Q6 // histocompatibility 2, Q region locus 6 // 17 B1|17 18.66	H2-Q6	5.83E-05	-2.28775
---		0.00047417	-2.287
NM_011627 // Tpbg // trophoblast glycoprotein // 9 E3.1|9 // 21983 /// ENSMUST000000065	Tpbg	1.19E-05	-2.28391
NM_001253804 // Slc12a4 // solute carrier family 12, member 4 // 8 D3|8 53.06 cM // 204	Slc12a4	7.46E-05	-2.28081
NM_001146318 // Cnp // 2,3-cyclic nucleotide 3 phosphodiesterase // 11 D|11 63.47 cM //	Cnp	0.000102373	-2.2788
NM_145447 // Mfsd7c // major facilitator superfamily domain containing 7C // 12 D2|12 /	Mfsd7c	0.000138417	-2.27326
ENSMUST00000132017 // Vps54 // vacuolar protein sorting 54 (yeast) // 11 A3|11 13.89 cM	Vps54	2.20E-05	-2.27251
NM_010757 // Mafk // v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (	Mafk	9.32E-06	-2.27247
NM_172894 // Ppp6r1 // protein phosphatase 6, regulatory subunit 1 // 7 A1|7 // 243819	Ppp6r1	1.84E-07	-2.27202
NM_198865 // Slitrk5 // SLIT and NTRK-like family, member 5 // 14|14 E3 // 75409 /// XM	Slitrk5	0.00341687	-2.27197
NM_001145979 // Gtpbp2 // GTP binding protein 2 // 17|17 C-D // 56055 /// NM_019581 //	Gtpbp2	6.53E-06	-2.27145
NM_011916 // Xrn1 // 5-3 exoribonuclease 1 // 9|9 E4 // 24127 /// ENSMUST00000034981 //	Xrn1	7.77E-06	-2.27023
NM_001276764 // Dst // dystonin // 1 B|1 12.91 cM // 13518 /// NM_010081 // Dst // dyst	Dst	0.00271654	-2.27001
NM_138953 // Ell2 // elongation factor RNA polymerase II 2 // 13 C1|13 // 192657 /// EN	Ell2	0.000231616	-2.26996
NM_153402 // Ago3 // argonaute RISC catalytic subunit 3 // 4 D2.2|4 // 214150 /// XM_00	Ago3	0.000315432	-2.26807
NM_009763 // Bst1 // bone marrow stromal cell antigen 1 // 5 B3|5 23.84 cM // 12182 ///	Bst1	4.95E-06	-2.26591
ENSMUST00000139214 // 4930430E12Rik // RIKEN cDNA 4930430E12 gene // --- // --- /// ENS	4930430E12Rik	5.40E-06	-2.26513
XM_006538385 // Gm11787 // predicted gene 11787 // 4 A1|4 // 666513 /// ENSMUST00000121	Gm11787	0.00026155	-2.26456
NM_027498 // Sik3 // SIK family kinase 3 // 9 A5.2|9 // 70661 /// ENSMUST00000120247 //	Sik3	4.74E-05	-2.26437
NM_145977 // Slc45a3 // solute carrier family 45, member 3 // 1 E4|1 // 212980 /// ENSM	Slc45a3	0.000170437	-2.26018
NM_008846 // Pip5k1b // phosphatidylinositol-4-phosphate 5-kinase, type 1 beta // 19|19	Pip5k1b	0.00515638	-2.25943
NM_007483 // Rhob // ras homolog gene family, member B // 12 A1.1|12 // 11852 /// ENSMU	Rhob	5.19E-06	-2.25859
NM_009943 // Cox6a2 // cytochrome c oxidase subunit VIa polypeptide 2 // 7 F3|7 70.04 c	Cox6a2	0.000985748	-2.25662
NR_035410 // Mir669k // microRNA 669k // 2|2 8.22 cM // 100316663 /// ENSMUST0000017774	Mir669k	0.00073378	-2.2529
ENSMUST00000102715 // Stk39 // serine/threonine kinase 39 // 2|2 C3 // 53416 /// BC0519	Stk39	0.00332107	-2.25195
NM_009910 // Cxcr3 // chemokine (C-X-C motif) receptor 3 // X D|X 44.58 cM // 12766 ///	Cxcr3	0.000840818	-2.24895
NM_011803 // Klf6 // Kruppel-like factor 6 // 13 A1|13 // 23849 /// ENSMUST00000000080	Klf6	8.13E-07	-2.24873
NR_033552 // Gm10125 // predicted gene 10125 // --- // 791318 /// ENSMUST00000161096 //	Gm10125	0.00447638	-2.248
---		0.00682687	-2.24559
---		0.00682687	-2.24559
ENSMUST00000157305 // Gm26048 // predicted gene, 26048 // --- // ---	Gm26048	0.00115545	-2.24405
NM_145931 // Zc3h7a // zinc finger CCCH type containing 7 A // 16 A1|16 // 106205 /// N	Zc3h7a	6.58E-06	-2.23798
ENSMUST00000140556 // Gm11206 // predicted gene 11206 // --- // --- /// AK053136 // Ada	Gm11206	3.59E-05	-2.2371
NM_028850 // Chic2 // cysteine-rich hydrophobic domain 2 // 5|5 D // 74277 /// ENSMUST0	Chic2	8.12E-09	-2.23453
NM_198642 // 5031414D18Rik // RIKEN cDNA 5031414D18 gene // 14 D3|14 // 271221 /// ENSM	5031414D18Rik	0.000537487	-2.22932
NM_008343 // Igfbp3 // insulin-like growth factor binding protein 3 // 11 A1|11 4.75 cM	Igfbp3	0.00618744	-2.22845
NM_007825 // Cyp7b1 // cytochrome P450, family 7, subfamily b, polypeptide 1 // 3 A1|3	Cyp7b1	0.000393202	-2.22807
NM_022028 // Sav1 // salvador homolog 1 (Drosophila) // 12|12 C3 // 64010 /// ENSMUST00	Sav1	4.47E-06	-2.22533
NM_026405 // Rab32 // RAB32, member RAS oncogene family // 10 A1|10 // 67844 /// ENSMUS	Rab32	1.35E-05	-2.22218
NM_018807 // Plagl2 // pleiomorphic adenoma gene-like 2 // 2|2 H2 // 54711 /// ENSMUST0	Plagl2	1.84E-05	-2.22067
NM_028283 // Uaca // uveal autoantigen with coiled-coil domains and ankyrin repeats //	Uaca	2.65E-05	-2.21961
NM_029749 // Usp42 // ubiquitin specific peptidase 42 // 5 G2|5 82.5 cM // 76800 /// XM	Usp42	1.53E-06	-2.21851
NM_023731 // Ccdc86 // coiled-coil domain containing 86 // 19 B|19 7.41 cM // 108673 //	Ccdc86	0.000752336	-2.21489
XM_006497832 // Psd4 // pleckstrin and Sec7 domain containing 4 // 2 A3|2 // 215632 ///	Psd4	0.000201774	-2.21377
---		0.00254822	-2.21364
NM_001170855 // Trim36 // tripartite motif-containing 36 // 18 C|18 24.41 cM // 28105 /	Trim36	0.00495473	-2.21311
ENSMUST00000119109 // Etv3 // ets variant 3 // 3 F1|3 // 27049 /// NM_001083318 // Etv3	Etv3	6.82E-06	-2.21093
XM_006529693 // A630001G21Rik // RIKEN cDNA A630001G21 gene // 1 C5|1 // 319997 /// XM_	A630001G21Rik	0.000182763	-2.20868
NM_001126047 // Sema4c // sema domain, immunoglobulin domain (Ig), transmembrane domain	Sema4c	0.0010019	-2.20786
NM_152804 // Plk2 // polo-like kinase 2 // 13|13 D2.1 // 20620 /// ENSMUST00000022212 /	Plk2	3.04E-06	-2.20744
NM_145373 // Sectm1a // secreted and transmembrane 1A // 11 E2|11 // 209588 /// XM_0065	Sectm1a	0.00029203	-2.20666
NM_001177785 // Cd44 // CD44 antigen // 2 E2|2 54.13 cM // 12505 /// NM_009851 // Cd44	Cd44	1.44E-06	-2.20084
NM_033541 // Oas1c // 2-5 oligoadenylate synthetase 1C // 5 F|5 60.64 cM // 114643 ///	Oas1c	4.07E-05	-2.19879
NM_030705 // Mesdc1 // mesoderm development candidate 1 // 7 D3|7 // 80889 /// ENSMUST0	Mesdc1	0.000476074	-2.19709
ENSMUST00000145372 // Gm15347 // predicted gene 15347 // --- // ---	Gm15347	0.000274216	-2.19655

NM_028791 // Cmtr1 // cap methyltransferase 1 // 17 A3.3|17 // 74157 /// ENSMUST0000002	Cmtr1	9.09E-06	-2.19537
NM_144880 // Ppp2r5a // protein phosphatase 2, regulatory subunit B, alpha // 1 H6|1 //	Ppp2r5a	1.06E-05	-2.19405
ENSMUST00000107254 // Rfx5 // regulatory factor X, 5 (influences HLA class II expressio	Rfx5	3.31E-05	-2.19392
---		0.00309587	-2.19264
NM_001083810 // Prr5l // proline rich 5 like // 2 E2|2 // 72446 /// NM_001110849 // Prr	Prr5l	0.000752878	-2.19138
ENSMUST00000163078 // Ms4a6b // membrane-spanning 4-domains, subfamily A, member 6B //	Ms4a6b	1.12E-05	-2.19091
NM_172133 // Adap2 // ArfGAP with dual PH domains 2 // 11 B5|11 47.56 cM // 216991 ///	Adap2	7.77E-06	-2.18916
NM_008506 // Mycl // v-myc myelocytomatosis viral oncogene homolog, lung carcinoma deri	Mycl	0.00528039	-2.18821
---		0.000421869	-2.18782
NM_016696 // Gpc1 // glypican 1 // 1 D|1 // 14733 /// XM_006529142 // Gpc1 // glypican	Gpc1	0.000107371	-2.18762
ENSMUST00000104261 // Gm23127 // predicted gene, 23127 // --- // --- /// AK163470 // El	Gm23127	0.00112951	-2.18624
ENSMUST00000166606 // Gm17092 // predicted gene 17092 // --- // ---	Gm17092	0.00320153	-2.18548
NM_001284503 // Cask // calcium/calmodulin-dependent serine protein kinase (MAGUK famil	Cask	0.000291833	-2.18494
NM_145501 // Pi4k2a // phosphatidylinositol 4-kinase type 2 alpha // 19 C3|19 35.74 cM	Pi4k2a	2.16E-05	-2.18237
ENSMUST00000122797 // Gm25292 // predicted gene, 25292 // --- // ---	Gm25292	0.000450445	-2.18055
NM_001039530 // Parp14 // poly (ADP-ribose) polymerase family, member 14 // 16 B3|16 //	Parp14	0.00236812	-2.18022
ENSMUST00000033900 // Rab20 // RAB20, member RAS oncogene family // 8 A1.1|8 5.73 cM //	Rab20	0.000159645	-2.17983
NR_029539 // Mir125a // microRNA 125a // 17|17 // 387235 /// ENSMUST00000083545 // Mir1	Mir125a	0.00229509	-2.17776
AK084985 // Gm10099 // predicted gene 10099 // --- // 791367	Gm10099	0.00430591	-2.1771
ENSMUST00000032429 // Med21 // mediator complex subunit 21 // 6 G3|6 77.7 cM // 108098	Med21	0.000266945	-2.17671
XM_006498189 // Pdss1 // prenyl (solanesyl) diphosphate synthase, subunit 1 // 2 A3|2 /	Pdss1	0.00440768	-2.17654
---		0.000129226	-2.17566
NM_001159318 // Il1rap // interleukin 1 receptor accessory protein // 16|16 B2 // 16180	Il1rap	0.00160796	-2.17541
NM_001139520 // Samhd1 // SAM domain and HD domain, 1 // 2|2 H2 // 56045 /// NM_018851	Samhd1	0.00016474	-2.17431
---		5.00E-05	-2.17363
NM_008247 // Ppap2a // phosphatidic acid phosphatase type 2A // 13 D2.2|13 // 19012 ///	Ppap2a	0.000125752	-2.17352
NM_001289593 // Kynu // kynureninase (L-kynurenine hydrolase) // 2|2 C1 // 70789 /// NM	Kynu	6.89E-05	-2.17075
NM_001033535 // Tnfaip8l3 // tumor necrosis factor, alpha-induced protein 8-like 3 // 9	Tnfaip8l3	0.00229495	-2.17021
NM_175136 // Rnf122 // ring finger protein 122 // 8 A3|8 // 68867 /// XM_006509189 // R	Rnf122	0.00106681	-2.16985
---		0.00211133	-2.16874
NM_001081175 // Itpkb // inositol 1,4,5-trisphosphate 3-kinase B // 1 H5|1 84.27 cM //	Itpkb	2.79E-06	-2.16793
NM_025541 // Asf1a // anti-silencing function 1A histone chaperone // 10 B3|10 // 66403	Asf1a	5.84E-05	-2.16711
NM_010799 // Minpp1 // multiple inositol polyphosphate histidine phosphatase 1 // 19 C1	Minpp1	1.04E-05	-2.16551
NM_133857 // Usp53 // ubiquitin specific peptidase 53 // 3|3 G3 // 99526 /// ENSMUST000	Usp53	0.000235766	-2.16506
---		0.000543646	-2.16394
---		0.00516157	-2.16068
NM_013822 // Jag1 // jagged 1 // 2 F3|2 67.73 cM // 16449 /// ENSMUST00000028735 // Jag	Jag1	5.46E-05	-2.16041
NM_133838 // Ehd4 // EH-domain containing 4 // 2 E5|2 // 98878 /// ENSMUST00000028755 /	Ehd4	0.000135581	-2.1601
NM_001040400 // Tet2 // tet methylcytosine dioxygenase 2 // 3 G3|3 // 214133 /// ENSMUS	Tet2	2.10E-05	-2.15969
NM_007395 // Acvr1b // activin A receptor, type 1B // 15 F2|15 56.48 cM // 11479 /// XM	Acvr1b	0.00456837	-2.15669
NM_001114664 // Iqsec2 // IQ motif and Sec7 domain 2 // X F3|X 68.46 cM // 245666 /// E	Iqsec2	0.000105667	-2.15653
---		0.000534393	-2.15232
---		0.00135901	-2.15142
NM_019577 // Ccl24 // chemokine (C-C motif) ligand 24 // 5|5 G1 // 56221 /// XM_0065044	Ccl24	0.00276187	-2.15067
NM_021525 // Rcl1 // RNA terminal phosphate cyclase-like 1 // 19 C1|19 // 59028 /// ENS	Rcl1	0.000137546	-2.15035
ENSMUST00000179566 // Gm6132 // predicted pseudogene 6132 // --- // ---	Gm6132	0.00579678	-2.14802
BC003781 // Ube2e1 // ubiquitin-conjugating enzyme E2E 1 // 14|14 A3 // 22194 /// NM_00	Ube2e1	0.000191353	-2.14627
NM_001164357 // Slc25a25 // solute carrier family 25 (mitochondrial carrier, phosphate	Slc25a25	0.00681602	-2.14592
NM_001081269 // Whsc1l1 // Wolf-Hirschhorn syndrome candidate 1-like 1 (human) // 8 A2|	Whsc1l1	7.92E-06	-2.1437
NM_026205 // Rnf151 // ring finger protein 151 // 17 A3.3|17 // 67504 /// ENSMUST000000	Rnf151	0.002558	-2.14315
ENSMUST00000169859 // Gm17542 // predicted gene, 17542 // --- // ---	Gm17542	0.000676133	-2.14269
NM_009192 // Sla // src-like adaptor // 15 D2|15 29.3 cM // 20491 /// ENSMUST0000010057	Sla	0.000434109	-2.14055
---		0.00139158	-2.13904
NM_001160251 // Zfp281 // zinc finger protein 281 // 1 E4|1 // 226442 /// NM_177643 //	Zfp281	2.82E-05	-2.13708
NM_001195632 // Arhgap32 // Rho GTPase activating protein 32 // 9 A4|9 // 330914 /// XM	Arhgap32	0.00441146	-2.13327
ENSMUST00000149688 // Mthfs // 5, 10-methenyltetrahydrofolate synthetase // 9 E3.1|9 //	Mthfs	0.000462576	-2.1331
NM_011464 // Spint2 // serine protease inhibitor, Kunitz type 2 // 7 B1|7 // 20733 ///	Spint2	0.00160529	-2.13227
NM_133224 // Atp13a1 // ATPase type 13A1 // 8 B3.3|8 // 170759 /// XM_006509564 // Atp1	Atp13a1	5.90E-07	-2.1255
---		0.000802589	-2.12403
NM_001039103 // Rasa4 // RAS p21 protein activator 4 // 5 G2|5 // 54153 /// NM_133914 /	Rasa4	8.52E-05	-2.12392
NM_001081127 // Adamts14 // a disintegrin-like and metallopeptidase (reprolysin type) w	Adamts14	0.00258158	-2.12334
NM_001130409 // Ptk2 // PTK2 protein tyrosine kinase 2 // 15 D3|15 33.94 cM // 14083 //	Ptk2	1.20E-05	-2.12326
NM_010637 // Klf4 // Kruppel-like factor 4 (gut) // 4 B3|4 29.76 cM // 16600 /// ENSMUS	Klf4	0.00371537	-2.12325
NM_133661 // Slc6a12 // solute carrier family 6 (neurotransmitter transporter, betaine/	Slc6a12	0.0011636	-2.12259
NM_001162465 // Dtnb // dystrobrevin, beta // 12 A1.1|12 1.88 cM // 13528 /// NM_007886	Dtnb	0.00395701	-2.12053
NM_198861 // Lrrc75a // leucine rich repeat containing 75A // 11 B2|11 // 192976 /// XM	Lrrc75a	1.14E-05	-2.11958
NM_198647 // Tbc1d22b // TBC1 domain family, member 22B // 17 A3.3|17 // 381085 /// ENS	Tbc1d22b	0.000102711	-2.11876
NM_001163014 // Gp6 // glycoprotein 6 (platelet) // 7 A1|7 // 243816 /// XM_006539909 /	Gp6	0.00465879	-2.11699
NM_001033310 // Cox18 // cytochrome c oxidase assembly protein 18 // 5 E1|5 // 231430 /	Cox18	2.90E-05	-2.11666
NM_011030 // P4ha1 // procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydr	P4ha1	2.04E-05	-2.11498
NM_007764 // Crkl // v-crk sarcoma virus CT10 oncogene homolog (avian)-like // 16 A3|16	Crkl	1.32E-05	-2.11471
---		0.000905674	-2.11464
NM_033524 // Spred1 // sprouty protein with EVH-1 domain 1, related sequence // 2 E5|2	Spred1	8.36E-05	-2.11319
NM_001159750 // Tcea1 // transcription elongation factor A (SII) 1 // 1 A1|1 // 21399 /	Tcea1	6.63E-05	-2.11152
NM_080575 // Acss1 // acyl-CoA synthetase short-chain family member 1 // 2 G3|2 // 6873	Acss1	3.55E-05	-2.11147
NM_011669 // Usp12 // ubiquitin specific peptidase 12 // 5|5 G2 // 22217 /// ENSMUST000	Usp12	0.000122171	-2.10955
NM_008136 // Gnl1 // guanine nucleotide binding protein-like 1 // 17 C-D|17 18.82 cM //	Gnl1	0.000240002	-2.1091
NM_001290504 // Mid1 // midline 1 // X and Y|X 79.19 cM // 17318 /// NM_001290505 // Mi	Mid1	0.000190971	-2.10712
NM_009807 // Casp1 // caspase 1 // 9 A1|9 2.46 cM // 12362 /// ENSMUST00000027015 // Ca	Casp1	0.000574646	-2.10687
NM_001005605 // Aebp2 // AE binding protein 2 // 6|6 G1 // 11569 /// NM_178803 // Aebp2	Aebp2	1.06E-05	-2.10664
NM_145834 // Il17c // interleukin 17C // 8 E1|8 // 234836 /// ENSMUST00000050963 // Il1	Il17c	0.00521711	-2.10369
NM_001003909 // Ankib1 // ankyrin repeat and IBR domain containing 1 // 5 A1|5 // 70797	Ankib1	1.37E-06	-2.10172
NM_001081194 // Kcnh4 // potassium voltage-gated channel, subfamily H (eag-related), me	Kcnh4	0.00684467	-2.10076
NM_001163283 // Zbtb5 // zinc finger and BTB domain containing 5 // 4 B1|4 // 230119 //	Zbtb5	0.000926799	-2.10035
NM_019788 // Bloc1s6 // biogenesis of lysosomal organelles complex-1, subunit 6, pallid	Bloc1s6	2.83E-05	-2.09963
ENSMUST00000052876 // Eva1b // eva-1 homolog B (C. elegans) // 4 D2.2|4 // 230752 /// N	Eva1b	3.48E-05	-2.0994
NM_007808 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063 /// ENSMUST000	Cycs	0.000658662	-2.09485
NM_001164671 // Dnaja1 // DnaJ (Hsp40) homolog, subfamily A, member 1 // 4 A5|4 // 1550	Dnaja1	2.06E-06	-2.09462
NM_144943 // Cd207 // CD207 antigen // 6|6 D1-D2 // 246278 /// ENSMUST00000037882 // Cd	Cd207	0.00106586	-2.09373

NM_133757 // Pgs1 // phosphatidylglycerophosphate synthase 1 // 11 E2|11 // 74451 /// X	Pgs1	0.000125692	-2.09251
NM_001127177 // Ptpn2 // protein tyrosine phosphatase, non-receptor type 2 // 18 E1|18	Ptpn2	0.000808082	-2.09185
NM_001079824 // Hnrnph3 // heterogeneous nuclear ribonucleoprotein H3 // 10 B4|10 // 43	Hnrnph3	0.000110272	-2.09177
NM_022018 // Fam129a // family with sequence similarity 129, member A // 1 G2|1 // 6391	Fam129a	9.96E-06	-2.09168
ENSMUST00000118518 // Gm12003 // predicted gene 12003 // --- // --- /// ENSMUST00000175	Gm12003	7.30E-05	-2.09135
AK191337 // Fam53c // family with sequence similarity 53, member C // 18 B1|18 // 66306	Fam53c	0.00208074	-2.09127
NM_001162941 // Mapre2 // microtubule-associated protein, RP/EB family, member 2 // 18	Mapre2	0.000263543	-2.08959
NM_009323 // Tbx15 // T-box 15 // 3 F2.2|3 43.03 cM // 21384 /// ENSMUST00000029462 //	Tbx15	0.000964077	-2.08858
NM_008689 // Nfkb1 // nuclear factor of kappa light polypeptide gene enhancer in B cell	Nfkb1	0.000780274	-2.08672
NM_010499 // Ier2 // immediate early response 2 // 8 C3|8 41.02 cM // 15936 /// ENSMUST	Ier2	5.70E-06	-2.08637
NM_019868 // Hnrnph2 // heterogeneous nuclear ribonucleoprotein H2 // X E3|X 56.2 cM //	Hnrnph2	0.00271606	-2.08347
NM_025480 // Tmem128 // transmembrane protein 128 // 5 B3|5 // 66309 /// XM_006504046 /	Tmem128	6.27E-05	-2.08315
---		0.00261059	-2.08235
NM_001081343 // 3110043O21Rik // RIKEN cDNA 3110043O21 gene // 4 A5|4 // 73205 /// XM_0	3110043O21Rik	4.19E-05	-2.08141
---		0.000134091	-2.08064
NM_001252662 // Dmtn // dematin actin binding protein // 14 D2|14 36.32 cM // 13829 ///	Dmtn	4.84E-05	-2.08052
NM_001080798 // Aff1 // AF4/FMR2 family, member 1 // 5 E|5 50.45 cM // 17355 /// NM_133	Aff1	3.02E-05	-2.07858
NM_008587 // Mertk // c-mer proto-oncogene tyrosine kinase // 2 F1|2 // 17289 /// ENSMU	Mertk	2.50E-06	-2.07811
NM_001111279 // Wdfy1 // WD repeat and FYVE domain containing 1 // 1|1 C4 // 69368 ///	Wdfy1	0.00373735	-2.07641
NM_015800 // Crim1 // cysteine rich transmembrane BMP regulator 1 (chordin like) // 17	Crim1	0.000240154	-2.07609
NM_029532 // Snrnp35 // small nuclear ribonucleoprotein 35 (U11/U12) // 5 F|5 // 76167	Snrnp35	0.000408912	-2.07537
NM_001205043 // Jarid2 // jumonji, AT rich interactive domain 2 // 13 A5|13 21.66 cM //	Jarid2	0.000414231	-2.07485
NM_001122594 // Phlpp2 // PH domain and leucine rich repeat protein phosphatase 2 // 8	Phlpp2	1.45E-05	-2.07237
ENSMUST00000150702 // Gm16292 // predicted gene 16292 // --- // ---	Gm16292	0.000775688	-2.07095
XR_106394 // A430060F13Rik // RIKEN cDNA A430060F13 gene // 11 D|11 // 100039739 /// XR	A430060F13Rik	0.00526677	-2.07025
NM_146252 // Tbc1d13 // TBC1 domain family, member 13 // 2 B|2 // 70296 /// XM_00649832	Tbc1d13	1.58E-05	-2.06952
NM_172630 // Mppe1 // metallophosphoesterase 1 // 18 E1|18 // 225651 /// XM_006525888 /	Mppe1	6.39E-05	-2.06675
NR_039585 // Mir5124a // microRNA 5124a // 13|13 20.13 cM // 100628630 /// ENSMUST00000	Mir5124a	0.000891131	-2.06488
NM_009887 // Cer1 // cerberus 1 homolog (Xenopus laevis) // 4 C3|4 39.4 cM // 12622 ///	Cer1	0.00157387	-2.06486
NM_008549 // Man2a1 // mannosidase 2, alpha 1 // 17|17 E1.2 // 17158 /// ENSMUST0000008	Man2a1	1.92E-06	-2.06427
ENSMUST00000104327 // Gm25878 // predicted gene, 25878 // --- // --- /// ENSMUST0000013	Gm25878	0.00179752	-2.06392
NM_024436 // Rab22a // RAB22A, member RAS oncogene family // 2 H4|2 97.26 cM // 19334 /	Rab22a	4.47E-06	-2.06323
NM_026968 // Manbal // mannosidase, beta A, lysosomal-like // 2 H1|2 // 69161 /// ENSMU	Manbal	2.87E-05	-2.06197
NR_040374 // A230028O05Rik // RIKEN cDNA A230028O05 gene // 16 B1|16 // 319487 /// ENSM	A230028O05Rik	0.000395331	-2.06173
NM_198006 // Coa5 // cytochrome C oxidase assembly factor 5 // 1 B|1 // 76178 /// ENSMU	Coa5	2.45E-06	-2.06129
---		0.00356456	-2.06066
NM_001167879 // Gareml // GRB2 associated, regulator of MAPK1-like // 5 B1|5 // 242915	Gareml	3.54E-05	-2.06014
NM_007986 // Fap // fibroblast activation protein // 2 C1.3|2 35.85 cM // 14089 /// XM_	Fap	0.00446644	-2.05958
NM_001163567 // Fam102b // family with sequence similarity 102, member B // 3 F3|3 // 3	Fam102b	9.44E-07	-2.05929
XM_006530302 // Trafd1 // TRAF type zinc finger domain containing 1 // 5 F|5 // 231712	Trafd1	2.54E-07	-2.05918
NM_153159 // Zc3h12a // zinc finger CCCH type containing 12A // 4 D2.2|4 // 230738 ///	Zc3h12a	0.000325035	-2.05646
NM_134063 // Fam208b // family with sequence similarity 208, member B // 13 A1|13 // 10	Fam208b	8.49E-06	-2.0546
NM_001025438 // Camk2d // calcium/calmodulin-dependent protein kinase II, delta // 3 G1	Camk2d	0.000424678	-2.05312
NM_001163703 // Dcun1d3 // DCN1, defective in cullin neddylation 1, domain containing 3	Dcun1d3	0.00450964	-2.05231
NM_001146268 // Pdgfrb // platelet derived growth factor receptor, beta polypeptide //	Pdgfrb	4.11E-06	-2.04805
NM_023670 // Igf2bp3 // insulin-like growth factor 2 mRNA binding protein 3 // 6 B2.3|6	Igf2bp3	0.00207322	-2.04788
---		0.00180068	-2.04688
NM_027642 // Phf6 // PHD finger protein 6 // X|X A4 // 70998 /// ENSMUST00000078944 //	Phf6	1.31E-05	-2.04348
ENSMUST00000070283 // Dennd1b // DENN/MADD domain containing 1B // 1 F|1 // 329260 ///	Dennd1b	0.000392025	-2.0412
---		0.000143293	-2.03976
ENSMUST00000146121 // Gm11292 // predicted gene 11292 // 13 A3.1|13 // 193453 /// AK042	Gm11292	0.000922778	-2.03808
AK157419 // Gm20100 // predicted gene, 20100 // 8|8 5.73 cM // 100504175	Gm20100	0.00276853	-2.03767
NM_001005507 // Smg7 // Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	Smg7	9.80E-06	-2.03719
NM_144920 // Plekha5 // pleckstrin homology domain containing, family A member 5 // 6 G	Plekha5	0.00012912	-2.03691
NM_001293772 // Palld // palladin, cytoskeletal associated protein // 8|8 B3.3 // 72333	Palld	0.00139209	-2.03517
NM_139311 // Mllt6 // myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Dr	Mllt6	0.00354713	-2.03497
NM_008029 // Flt4 // FMS-like tyrosine kinase 4 // 11 A5-B1|11 29.69 cM // 14257 /// EN	Flt4	0.00237047	-2.03416
NM_001168277 // Jazf1 // JAZF zinc finger 1 // 6 B3|6 25.74 cM // 231986 /// NM_173406	Jazf1	0.00384643	-2.03077
---		0.000449525	-2.02765
---		0.00409317	-2.02594
NM_178607 // Rnf24 // ring finger protein 24 // 2 F1|2 63.32 cM // 51902 /// ENSMUST000	Rnf24	0.00598674	-2.02382
---		0.0006979	-2.02161
NM_001113330 // Crx // cone-rod homeobox // 7 A2|7 8.6 cM // 12951 /// NM_007770 // Crx	Crx	6.35E-05	-2.02048
NM_011669 // Usp12 // ubiquitin specific peptidase 12 // 5|5 G2 // 22217 /// ENSMUST000	Usp12	1.31E-05	-2.01967
NM_027715 // Otud1 // OTU domain containing 1 // 2 A3|2 // 71198 /// ENSMUST00000052168	Otud1	0.000403725	-2.01494
ENSMUST00000038287 // Dusp5 // dual specificity phosphatase 5 // 19 D2|19 // 240672 ///	Dusp5	5.20E-05	-2.0115
NM_001290413 // Traf2 // TNF receptor-associated factor 2 // 2 A3|2 // 22030 /// NM_009	Traf2	0.000106918	-2.00875
NM_178920 // Mal2 // mal, T cell differentiation protein 2 // 15 D1|15 // 105853 /// EN	Mal2	0.000244146	-2.00869
---		0.000100489	-2.00782
NM_001033439 // Lrch1 // leucine-rich repeats and calponin homology (CH) domain contain	Lrch1	1.09E-08	-2.00762
---		0.00223445	-2.00684
XR_381025 // LOC102639588 // uncharacterized LOC102639588 // --- // 102639588 /// ENSMU	LOC102639588	0.00464431	-2.00605
---		0.000299129	-2.00356
ENSMUST00000114996 // Optn // optineurin // 2 A1|2 3.15 cM // 71648 /// NM_181848 // Op	Optn	2.21E-05	-2.00287
NM_133190 // Cacng8 // calcium channel, voltage-dependent, gamma subunit 8 // 7 A1|7 1.	Cacng8	0.0037822	-2.00287
NM_009696 // Apoe // apolipoprotein E // 7 A3|7 9.94 cM // 11816 /// ENSMUST00000174064	Apoe	9.71E-07	2.00001
ENSMUST00000141023 // Gm13609 // predicted gene 13609 // --- // --- /// XR_399674 // LO	Gm13609	0.00606043	2.00033
BC060304 // Hist1h2bg // histone cluster 1, H2bg // 13 A2-A3|13 // 319181	Hist1h2bg	0.000689603	2.00166
NM_001253897 // Ecsit // ECSIT homolog (Drosophila) // 9|9 A4 // 26940 /// NM_001253898	Ecsit	0.000337805	2.00207
NM_001289458 // Hgf // hepatocyte growth factor // 5 A2-A3|5 7.07 cM // 15234 /// NM_00	Hgf	0.000157874	2.00282
NM_001166635 // Mid1ip1 // Mid1 interacting protein 1 (gastrulation specific G12-like (	Mid1ip1	0.000520363	2.00295
NM_134255 // Elovl5 // ELOVL family member 5, elongation of long chain fatty acids (yea	Elovl5	6.96E-06	2.00326
---		0.000669431	2.00349
NM_001167691 // Sirt4 // sirtuin 4 // 5 F|5 // 75387 /// NM_133760 // Sirt4 // sirtuin	Sirt4	5.88E-05	2.00433
NM_026536 // Atp5s // ATP synthase, H+ transporting, mitochondrial F0 complex, subunit	Atp5s	0.00314245	2.00453
NM_007444 // Amd2 // S-adenosylmethionine decarboxylase 2 // 10 B1|10 // 100041585 ///	Amd2	2.30E-05	2.00454
NM_205820 // Tlr13 // toll-like receptor 13 // X D|X // 279572 /// ENSMUST00000040065 /	Tlr13	2.90E-06	2.00486
NM_172988 // Fbxl4 // F-box and leucine-rich repeat protein 4 // 4 A3|4 // 269514 /// N	Fbxl4	0.000111174	2.00606
NM_019747 // Zfp113 // zinc finger protein 113 // 5|5 G1 // 56314 /// ENSMUST0000004939	Zfp113	0.00237314	2.0068

---		0.000762576	2.00777
NM_001204906 // Recql // RecQ protein-like // 6 G2|6 73.91 cM // 19691 /// NM_001204907	Recql	7.75E-06	2.00807
NM_026602 // Bcas2 // breast carcinoma amplified sequence 2 // 3 F2.2|3 // 68183 /// XM	Bcas2	8.03E-07	2.00843
ENSMUST00000032967 // Lipt2 // lipoyl(octanoyl) transferase 2 (putative) // 7|7 F1 // 6	Lipt2	0.00259266	2.00916
---		0.00414934	2.00925
NM_145398 // Casd1 // CAS1 domain containing 1 // 6 A1|6 1.81 cM // 213819 /// XM_00650	Casd1	2.43E-05	2.01072
NM_001033145 // 1190002N15Rik // RIKEN cDNA 1190002N15 gene // 9 E3.3|9 // 68861 /// EN	1190002N15Rik	0.000155497	2.01109
XM_006511619 // Mapkapk3 // mitogen-activated protein kinase-activated protein kinase 3	Mapkapk3	7.72E-05	2.01148
NM_007924 // Ell // elongation factor RNA polymerase II // 8 C1|8 // 13716 /// ENSMUST0	Ell	0.000366188	2.01176
NM_009706 // Arhgap5 // Rho GTPase activating protein 5 // 12 C1|12 22.16 cM // 11855 /	Arhgap5	0.00330272	2.01389
NM_001164173 // Cpsf1 // cleavage and polyadenylation specific factor 1 // 15 D3|15 //	Cpsf1	6.13E-07	2.01401
---		0.000474149	2.01405
NM_001110251 // Hmbs // hydroxymethylbilane synthase // 9 A5.2|9 24.84 cM // 15288 ///	Hmbs	0.00124563	2.01489
NM_001190984 // Lancl1 // LanC (bacterial lantibiotic synthetase component C)-like 1 //	Lancl1	0.0025499	2.01496
NM_001130150 // Arhgef1 // Rho guanine nucleotide exchange factor (GEF) 1 // 7 A3|7 //	Arhgef1	2.94E-05	2.01573
---		0.00317865	2.01612
NM_145415 // Diexf // digestive organ expansion factor homolog (zebrafish) // 1 H6|1 //	Diexf	9.06E-05	2.01636
NR_027897 // 0610012G03Rik // RIKEN cDNA 0610012G03 gene // 16 B2|16 // 106264 /// BC02	0610012G03Rik	0.000177354	2.01706
NM_175528 // E330009J07Rik // RIKEN cDNA E330009J07 gene // 6 B1|6 // 243780 /// ENSMUS	E330009J07Rik	0.00138016	2.01729
NM_027810 // Bbs7 // Bardet-Biedl syndrome 7 (human) // 3 B|3 // 71492 /// ENSMUST00000	Bbs7	0.000379042	2.0173
NM_008563 // Mcm3 // minichromosome maintenance deficient 3 (S. cerevisiae) // 1|1 A3-A	Mcm3	5.32E-05	2.01778
---		0.000671249	2.01882
NM_023831 // Ift46 // intraflagellar transport 46 // 9 A5.2|9 // 76568 /// XM_006510671	Ift46	0.00010633	2.0195
NM_153116 // Gtpbp10 // GTP-binding protein 10 (putative) // 5 A1|5 // 207704 /// ENSMU	Gtpbp10	0.00149369	2.02064
NM_001033298 // Kiz // kizuna centrosomal protein // 2 G2|2 // 228730 /// XM_006499299	Kiz	0.00051476	2.02147
ENSMUST00000145438 // 2810008D09Rik // RIKEN cDNA 2810008D09 gene // 11|11 // 76972 ///	2810008D09Rik	0.00195971	2.02275
NM_145466 // Ggact // gamma-glutamylamine cyclotransferase // 14 E5|14 // 223267 /// XM	Ggact	0.00175495	2.02312
NM_025615 // 2810004N23Rik // RIKEN cDNA 2810004N23 gene // 8 E2|8 // 66523 /// ENSMUST	2810004N23Rik	0.00350684	2.02376
NM_001291031 // Ap5s1 // adaptor-related protein 5 complex, sigma 1 subunit // 2|2 F3 /	Ap5s1	0.000454111	2.02413
NM_026246 // Mrpl49 // mitochondrial ribosomal protein L49 // 19 A|19 4.34 cM // 18120	Mrpl49	2.31E-05	2.02513
NM_001253904 // Ncor2 // nuclear receptor co-repressor 2 // 5 F|5 // 20602 /// NM_00125	Ncor2	0.000292298	2.02536
NM_133227 // Nup155 // nucleoporin 155 // 15|15 A2 // 170762 /// XM_006519972 // Nup155	Nup155	4.90E-06	2.02596
NM_001162855 // Nsmce4a // non-SMC element 4 homolog A (S. cerevisiae) // 7 F3|7 // 678	Nsmce4a	5.78E-07	2.02611
NM_001285997 // Prc1 // protein regulator of cytokinesis 1 // 7 D3|7 45.62 cM // 233406	Prc1	0.000341345	2.02648
NM_009086 // Polr1b // polymerase (RNA) I polypeptide B // 2 F3|2 // 20017 /// ENSMUST0	Polr1b	0.00677467	2.02694
---		0.00446899	2.02699
NM_033320 // Glce // glucuronyl C5-epimerase // 9 C-D|9 // 93683 /// ENSMUST00000034785	Glce	0.000106523	2.02728
NM_025346 // Rmnd5b // required for meiotic nuclear division 5 homolog B (S. cerevisiae	Rmnd5b	2.25E-05	2.02731
NM_172597 // Txndc16 // thioredoxin domain containing 16 // 14|14 C1 // 70561 /// XM_00	Txndc16	6.23E-05	2.02813
NM_172809 // Sacs // sacsin // 14 D1|14 32.13 cM // 50720 /// ENSMUST00000089394 // Sac	Sacs	0.0013325	2.0286
NM_027334 // Mettl7a1 // methyltransferase like 7A1 // 15|15 F3 // 70152 /// XM_0065213	Mettl7a1	0.000353439	2.02964
XM_006511927 // Ctnnb1 // catenin (cadherin associated protein), beta 1 // 9 F4|9 72.19	Ctnnb1	1.61E-06	2.03066
NM_008961 // Pter // phosphotriesterase related // 2 A1|2 // 19212 /// XM_006497400 //	Pter	0.000413794	2.0308
NM_021434 // Gpr180 // G protein-coupled receptor 180 // 14 E4|14 // 58245 /// ENSMUST0	Gpr180	0.000492318	2.03085
NM_028320 // Adipor1 // adiponectin receptor 1 // 1 E4|1 // 72674 /// ENSMUST0000002772	Adipor1	1.57E-06	2.03199
NM_178653 // Sccpdh // saccharopine dehydrogenase (putative) // 1 H4|1 // 109232 /// EN	Sccpdh	0.000301652	2.03236
NM_001146329 // Sbk2 // SH3-binding domain kinase family, member 2 // 7 A1|7 // 381836	Sbk2	0.0022511	2.03257
NM_177741 // Ppp1r3b // protein phosphatase 1, regulatory (inhibitor) subunit 3B // 8 A	Ppp1r3b	0.0023323	2.0326
---		0.00149888	2.03284
NM_177721 // Ranbp6 // RAN binding protein 6 // 19 C1|19 // 240614 /// ENSMUST0000000995	Ranbp6	0.00330545	2.03376
---		0.00616102	2.03382
NM_027456 // Armc9 // armadillo repeat containing 9 // 1 C5|1 // 78795 /// NM_030184 //	Armc9	0.00185325	2.03489
NM_021028 // Tk2 // thymidine kinase 2, mitochondrial // 8 D3|8 // 57813 /// NR_045642	Tk2	5.15E-05	2.03683
NM_177843 // Gm14461 // predicted gene 14461 // 2 C3|2 // 329436 /// ENSMUST00000067618	Gm14461	0.00526977	2.03773
NM_009194 // Slc12a2 // solute carrier family 12, member 2 // 18 D3|18 32.15 cM // 2049	Slc12a2	0.000178564	2.03797
ENSMUST00000052645 // Nudt6 // nudix (nucleoside diphosphate linked moiety X)-type moti	Nudt6	0.000324925	2.03826
NM_001252547 // Sh2d3c // SH2 domain containing 3C // 2 B|2 // 27387 /// NM_013781 // S	Sh2d3c	0.000120945	2.03827
---		7.75E-05	2.03904
NM_025642 // Mis18a // MIS18 kinetochore protein homolog A (S. pombe) // 16 C3.3|16 //	Mis18a	6.81E-05	2.03934
NM_009690 // Cd5l // CD5 antigen-like // 3 F1|3 // 11801 /// ENSMUST00000015998 // Cd5l	Cd5l	1.23E-05	2.03975
NM_133719 // Metrn // meteorin, glial cell differentiation regulator // 17 A3.3|17 // 7	Metrn	0.00103921	2.03983
NM_009791 // Aspm // asp (abnormal spindle)-like, microcephaly associated (Drosophila)	Aspm	0.00663184	2.0402
NM_020584 // Terf2ip // telomeric repeat binding factor 2, interacting protein // 8 E1|	Terf2ip	0.000179223	2.04063
NM_001114339 // Pank1 // pantothenate kinase 1 // 19 G1-G3|19 // 75735 /// NM_023792 //	Pank1	1.13E-05	2.04117
NM_183186 // Foxn3 // forkhead box N3 // 12 E|12 // 71375 /// XM_006516236 // Foxn3 //	Foxn3	3.40E-05	2.04144
NM_172151 // Zdhhc8 // zinc finger, DHHC domain containing 8 // 16 A3|16 11.29 cM // 27	Zdhhc8	0.000516	2.04164
NM_011274 // Uri1 // URI1, prefoldin-like chaperone // 7 B2|7 // 19777 /// XM_006539676	Uri1	0.00015379	2.04273
---		0.00132579	2.04276
NM_009663 // Alox5ap // arachidonate 5-lipoxygenase activating protein // 5 G3|5 // 116	Alox5ap	2.44E-07	2.04283
NM_001243741 // C87436 // expressed sequence C87436 // 6 D1|6 // 232196 /// XM_00650597	C87436	0.00120011	2.04332
NM_009272 // Srm // spermidine synthase // 4 E2|4 // 20810 /// ENSMUST00000006611 // Sr	Srm	0.000207993	2.04374
NM_001164480 // Sipa1 // signal-induced proliferation associated gene 1 // 19 A|19 4.34	Sipa1	8.83E-05	2.04418
NM_018889 // Pigb // phosphatidylinositol glycan anchor biosynthesis, class B // 9 D|9	Pigb	5.41E-05	2.04471
NM_019993 // Aldh9a1 // aldehyde dehydrogenase 9, subfamily A1 // 1|1 H2 // 56752 /// X	Aldh9a1	5.93E-06	2.04475
NM_198607 // Them6 // thioesterase superfamily member 6 // 15|15 E1 // 223626 /// ENSMU	Them6	0.00674648	2.04514
NR_028564 // Snord95 // small nucleolar RNA, C/D box 95 // 11|11 // 100216540 /// ENSMU	Snord95	0.00376783	2.04541
NM_198306 // Galnt9 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosa	Galnt9	0.000895172	2.04544
NM_001290181 // Nudt7 // nudix (nucleoside diphosphate linked moiety X)-type motif 7 //	Nudt7	0.000550697	2.04786
ENSMUST00000109020 // Gm14440 // predicted gene 14440 // 2|2 // 100503353 /// ENSMUST00	Gm14440	3.32E-06	2.04805
NM_028410 // Prkrir // protein-kinase, interferon-inducible double stranded RNA depende	Prkrir	0.000206564	2.04846
NM_027206 // Tnfaip8l2 // tumor necrosis factor, alpha-induced protein 8-like 2 // 3 F2	Tnfaip8l2	4.13E-05	2.04932
NM_013512 // Epb4.1l4a // erythrocyte protein band 4.1-like 4a // 18 B1|18 // 13824 ///	Epb4.1l4a	0.000142722	2.04958
NM_001252316 // Shmt2 // serine hydroxymethyltransferase 2 (mitochondrial) // 10 D3|10	Shmt2	0.000585282	2.05001
NM_001206335 // Itfg3 // integrin alpha FG-GAP repeat containing 3 // 17 A3.3|17 // 106	Itfg3	1.97E-06	2.05072
XM_006514336 // Dtx3 // deltex 3 homolog (Drosophila) // 10 D3|10 // 80904 /// ENSMUST0	Dtx3	1.48E-05	2.05177
NM_001199188 // Snx5 // sorting nexin 5 // 2 H1|2 70.98 cM // 69178 /// NM_024225 // Sn	Snx5	3.19E-07	2.05189
NM_028101 // Jmjd8 // jumonji domain containing 8 // 17|17 B1 // 72106 /// ENSMUST00000	Jmjd8	0.000112736	2.05312
NM_009811 // Casp6 // caspase 6 // 3|3 H1 // 12368 /// ENSMUST00000029626 // Casp6 // c	Casp6	0.000922718	2.05338
NM_173757 // Mrps27 // mitochondrial ribosomal protein S27 // 13 D1|13 // 218506 /// EN	Mrps27	0.000501275	2.05383

NM_001168240 // Irak1bp1 // interleukin-1 receptor-associated kinase 1 binding protein	Irak1bp1	0.000118358	2.05435
NM_024248 // Cars2 // cysteinyl-tRNA synthetase 2 (mitochondrial)(putative) // 8|8 A2 /	Cars2	2.49E-05	2.05467
NM_026632 // Rpa3 // replication protein A3 // 6 A1|6 // 68240 /// XM_885368 // Gm6195	Rpa3	0.00533654	2.05527
ENSMUST00000132370 // 4933439K11Rik // RIKEN cDNA 4933439K11 gene // 1|1 // 71319 /// E	4933439K11Rik	0.00246676	2.05572
NR_027866 // 5730408K05Rik // RIKEN cDNA 5730408K05 gene // 19|19 // 67531 /// NR_03959	5730408K05Rik	0.00255158	2.0565
NM_028314 // 2700097O09Rik // RIKEN cDNA 2700097O09 gene // 12 C1|12 // 72658 /// NR_03	2700097O09Ril	0.00329389	2.05689
NM_001163241 // Nqo2 // NAD(P)H dehydrogenase, quinone 2 // 13 A4|13 14.01 cM // 18105	Nqo2	7.38E-05	2.05743
NM_029701 // Spcs3 // signal peptidase complex subunit 3 homolog (S. cerevisiae) // 8 B	Spcs3	1.06E-05	2.05771
NM_026430 // Uxs1 // UDP-glucuronate decarboxylase 1 // 1 C1.1|1 // 67883 /// XM_006496	Uxs1	0.00168531	2.05857
NM_013865 // Ndrg3 // N-myc downstream regulated gene 3 // 2 H1|2 // 29812 /// NM_18095	Ndrg3	1.59E-06	2.05864
NM_001163819 // Fance // Fanconi anemia, complementation group E // 17 A3.3|17 // 72775	Fance	0.00454727	2.05989
NM_172770 // Ttc12 // tetratricopeptide repeat domain 12 // 9 A5.3|9 // 235330 /// ENSM	Ttc12	4.83E-07	2.05993
NM_080793 // Setd7 // SET domain containing (lysine methyltransferase) 7 // 3 C|3 // 73	Setd7	0.000144995	2.06009
NM_001134384 // Iqsec1 // IQ motif and Sec7 domain 1 // 6 D1|6 40.16 cM // 232227 /// X	Iqsec1	0.000160105	2.06011
NM_139236 // Nol6 // nucleolar protein family 6 (RNA-associated) // 4 A5|4 // 230082 //	Nol6	4.97E-06	2.06256
NM_172742 // Mtmr10 // myotubularin related protein 10 // 7 C|7 // 233315 /// ENSMUST00	Mtmr10	6.84E-06	2.06281
NM_001164420 // Pqlc1 // PQ loop repeat containing 1 // 18 E3|18 // 66943 /// NM_001164	Pqlc1	3.69E-06	2.06306
NM_145624 // Zfp709 // zinc finger protein 709 // 8 B3.3|8 // 236193	Zfp709	0.0025292	2.06322
NM_011947 // Map3k3 // mitogen-activated protein kinase kinase kinase 3 // 11 E1|11 //	Map3k3	1.31E-06	2.06378
XM_006541085 // 2410002F23Rik // RIKEN cDNA 2410002F23 gene // 7 B4|7 // 668661 /// ENS	2410002F23Rik	7.01E-06	2.06532
NM_001276446 // Alad // aminolevulinate, delta-, dehydratase // 4 B3|4 33.17 cM // 1702	Alad	0.000323114	2.06534
NM_011912 // Vax2 // ventral anterior homeobox 2 // 6 C3|6 35.94 cM // 24113 /// ENSMUS	Vax2	0.00540525	2.06665
NM_008892 // Pola1 // polymerase (DNA directed), alpha 1 // X C-D|X 41.06 cM // 18968 /	Pola1	0.000540421	2.0667
NM_001163126 // Cog5 // component of oligomeric golgi complex 5 // 12 A2|12 // 238123 /	Cog5	5.67E-07	2.06733
ENSMUST00000181224 // AU020206 // expressed sequence AU020206 // --- // --- /// AK04941	AU020206	4.75E-08	2.06781
NM_026796 // Smyd2 // SET and MYND domain containing 2 // 1 H6|1 // 226830 /// XM_00649	Smyd2	0.000484335	2.06822
NM_001082476 // Ndor1 // NADPH dependent diflavin oxidoreductase 1 // 2 A3|2 // 78797 /	Ndor1	7.29E-06	2.06836
NM_001285980 // Skp2 // S-phase kinase-associated protein 2 (p45) // 15 A2|15 // 27401	Skp2	2.81E-05	2.0691
NM_009478 // Urod // uroporphyrinogen decarboxylase // 4 D1|4 53.41 cM // 22275 /// XM_	Urod	1.80E-05	2.06967
NM_029115 // Ccdc181 // coiled-coil domain containing 181 // 1|1 H1 // 74895 /// ENSMUS	Ccdc181	0.0003442	2.07005
---		0.00196138	2.07008
XM_006497827 // Surf2 // surfeit gene 2 // 2 A3|2 19.1 cM // 20931 /// ENSMUST000000150	Surf2	4.20E-06	2.07011
NM_001286544 // Ccpg1 // cell cycle progression 1 // 9 D|9 40.08 cM // 72278 /// ENSMUS	Ccpg1	0.000221482	2.07103
NM_023733 // Crot // carnitine O-octanoyltransferase // 5 A1|5 // 74114 /// ENSMUST0000	Crot	1.17E-05	2.07292
ENSMUST00000103130 // Dsn1 // DSN1, MIND kinetochore complex component, homolog (S. cer	Dsn1	0.00592051	2.07347
NM_028284 // Bbs5 // Bardet-Biedl syndrome 5 (human) // 2|2 C3 // 72569 /// ENSMUST0000	Bbs5	7.35E-05	2.07428
NM_026268 // Dusp6 // dual specificity phosphatase 6 // 10|10 C3 // 67603 /// ENSMUST00	Dusp6	7.00E-07	2.07564
NM_001285893 // Vps8 // vacuolar protein sorting 8 homolog (S. cerevisiae) // 16 B1|16	Vps8	1.05E-06	2.07567
NM_025671 // Ogfod2 // 2-oxoglutarate and iron-dependent oxygenase domain containing 2	Ogfod2	0.00380381	2.07587
NR_045299 // 2900076A07Rik // RIKEN cDNA 2900076A07 gene // 7 D1|7 // 100504421 /// ENS	2900076A07Rik	0.00169859	2.0764
NM_026046 // Zfp329 // zinc finger protein 329 // 7|7 A2 // 67230 /// ENSMUST0000007222	Zfp329	8.53E-05	2.07737
NM_133683 // Tmem19 // transmembrane protein 19 // 10 D2|10 // 67226 /// XM_006513974 /	Tmem19	0.000287076	2.0779
NM_025677 // Tsen15 // tRNA splicing endonuclease 15 homolog (S. cerevisiae) // 1 G3|1	Tsen15	0.00345878	2.0787
NM_001293791 // Ints10 // integrator complex subunit 10 // 8|8 C1 // 70885 /// NM_00129	Ints10	1.26E-05	2.07961
NM_199068 // Foxk1 // forkhead box K1 // 5 G2|5 81.53 cM // 17425 /// ENSMUST0000007283	Foxk1	0.000885948	2.08063
NM_183046 // Kif20b // kinesin family member 20B // 19 C2|19 // 240641 /// ENSMUST00000	Kif20b	6.74E-05	2.08068
NM_001005860 // Clec4a4 // C-type lectin domain family 4, member a4 // 6 F2|6 // 474145	Clec4a4	0.000156672	2.08147
NM_001099349 // Gm14308 // predicted gene 14308 // 2 H4|2 // 100043381 /// NM_001100415	Gm14308	1.64E-07	2.0818
NM_028634 // Cby1 // chibby homolog 1 (Drosophila) // 15 E2|15 // 73739 /// XM_00652148	Cby1	0.000104668	2.0821
NM_026044 // Dph7 // diphthamine biosynethesis 7 // 2 A3|2 // 67228 /// XM_006498242 //	Dph7	0.00394214	2.08439
NM_001285991 // Tbc1d5 // TBC1 domain family, member 5 // 17 C|17 // 72238 /// NM_00128	Tbc1d5	4.54E-05	2.0846
NM_019998 // Alg2 // asparagine-linked glycosylation 2 (alpha-1,3-mannosyltransferase)	Alg2	6.57E-06	2.08537
NM_001285487 // Mknk1 // MAP kinase-interacting serine/threonine kinase 1 // 4 D1|4 //	Mknk1	6.15E-05	2.08558
NM_008513 // Lrp5 // low density lipoprotein receptor-related protein 5 // 19|19 B // 1	Lrp5	0.000139443	2.0871
NM_001110350 // Sin3a // transcriptional regulator, SIN3A (yeast) // 9 B|9 30.89 cM //	Sin3a	2.06E-05	2.08713
NM_011630 // Nr2c2 // nuclear receptor subfamily 2, group C, member 2 // 6 D1|6 // 2202	Nr2c2	4.75E-05	2.08742
NM_001289630 // Mgme1 // mitochondrial genome maintainance exonuclease 1 // 2|2 H1 // 7	Mgme1	0.00104106	2.08759
NM_199198 // Hdac10 // histone deacetylase 10 // 15 E3|15 // 170787 /// NR_028447 // Hd	Hdac10	0.00182919	2.09027
NM_010864 // Myo5a // myosin VA // 9 D|9 42.26 cM // 17918 /// ENSMUST00000123128 // My	Myo5a	3.76E-07	2.09041
NM_010322 // Gnpat // glyceronephosphate O-acyltransferase // 8 E2|8 72.81 cM // 14712	Gnpat	2.38E-06	2.09155
XM_006530467 // 2210016L21Rik // RIKEN cDNA 2210016L21 gene // 5 F|5 // 72357 /// ENSMU	2210016L21Rik	6.61E-05	2.09285
NM_001008502 // Bbs12 // Bardet-Biedl syndrome 12 (human) // 3 B|3 // 241950 /// NM_001	Bbs12	0.00473768	2.09307
ENSMUST00000146409 // Slc26a2 // solute carrier family 26 (sulfate transporter), member	Slc26a2	0.000270096	2.09311
NM_025411 // Pithd1 // PITH (C-terminal proteasome-interacting domain of thioredoxin-li	Pithd1	0.00410308	2.09327
NM_019482 // Panx1 // pannexin 1 // 9 A2|9 // 55991 /// ENSMUST00000056755 // Panx1 //	Panx1	2.13E-06	2.09333
NM_001293630 // Slc37a4 // solute carrier family 37 (glucose-6-phosphate transporter),	Slc37a4	0.000343175	2.09421
NM_008026 // Fli1 // Friend leukemia integration 1 // 9 A4|9 17.74 cM // 14247 /// XM_0	Fli1	4.64E-06	2.09437
NM_001277898 // Prkaca // protein kinase, cAMP dependent, catalytic, alpha // 8|8 C3 //	Prkaca	2.18E-05	2.09482
NM_008702 // Nlk // nemo like kinase // 11 B5|11 // 18099 /// ENSMUST00000142739 // Nlk	Nlk	2.56E-06	2.09501
NM_130449 // Colec12 // collectin sub-family member 12 // 18 A1|18 // 140792 /// ENSMUS	Colec12	1.19E-06	2.09764
ENSMUST00000120226 // Cdk4 // cyclin-dependent kinase 4 // 10 D3|10 // 12567 /// ENSMUS	Cdk4	3.93E-07	2.09805
NM_001293800 // Ocel1 // occludin/ELL domain containing 1 // 8|8 C1 // 77090 /// NM_029	Ocel1	0.000306017	2.09825
NM_008149 // Gpam // glycerol-3-phosphate acyltransferase, mitochondrial // 19 D2|19 50	Gpam	0.000395016	2.0985
NM_175563 // Prr11 // proline rich 11 // 11 C|11 // 270906 /// ENSMUST00000051395 // Pr	Prr11	0.00224667	2.09912
NM_025659 // Abi3 // ABI gene family, member 3 // 11 D|11 // 66610 /// XM_006533953 //	Abi3	8.34E-05	2.09944
NM_179203 // Atad3a // ATPase family, AAA domain containing 3A // 4 E2|4 // 108888 ///	Atad3a	0.000519508	2.09949
NM_025904 // Yae1d1 // Yae1 domain containing 1 // 13 A2-A3|13 // 67008 /// ENSMUST0000	Yae1d1	0.00384275	2.09996
NM_025812 // Hmg20a // high mobility group 20A // 9|9 C // 66867 /// XM_006511368 // Hm	Hmg20a	9.06E-06	2.10144
NM_001167994 // Trmt2b // TRM2 tRNA methyltransferase 2B // X E3|X // 215201 /// NM_172	Trmt2b	8.89E-05	2.10163
NM_001136090 // Poli // polymerase (DNA directed), iota // 18 E2|18 44.48 cM // 26447 /	Poli	5.38E-05	2.10219
NM_009875 // Cdkn1b // cyclin-dependent kinase inhibitor 1B // 6 G1|6 65.77 cM // 12576	Cdkn1b	3.83E-06	2.10462
NM_008354 // Il12rb2 // interleukin 12 receptor, beta 2 // 6 C1|6 30.81 cM // 16162 ///	Il12rb2	0.00649988	2.10518
NM_001099327 // Gm14305 // predicted gene 14305 // 2 H4|2 // 100043387 /// NM_001099349	Gm14305	8.18E-08	2.10667
NM_008234 // Hells // helicase, lymphoid specific // 19|19 C3-D1 // 15201 /// XM_006526	Hells	0.000788542	2.10724
NM_013546 // Hebp1 // heme binding protein 1 // 6 G1|6 // 15199 /// ENSMUST00000045855	Hebp1	2.03E-06	2.10745
XM_006509478 // 4933411K20Rik // RIKEN cDNA 4933411K20 gene // 8 B2|8 26.16 cM // 66756	4933411K20Rik	8.86E-05	2.10829
NM_025633 // Metap1d // methionyl aminopeptidase type 1D (mitochondrial) // 2 C2|2 // 6	Metap1d	0.000392636	2.10904
NM_010517 // Igfbp4 // insulin-like growth factor binding protein 4 // 11 D|11 // 16010	Igfbp4	4.72E-05	2.10976
NM_016658 // Galt // galactose-1-phosphate uridyl transferase // 4 A5|4 22.07 cM // 144	Galt	0.000672783	2.11001

ENSMUST00000119830 // Zfp740 // zinc finger protein 740 // 15 F3|15 // 68744 /// ENSMUS	Zfp740	3.83E-06	2.11039
---		0.00126946	2.11054
XM_006504587 // Nxpe5 // neurexophilin and PC-esterase domain family, member 5 // 5 G2|	Nxpe5	0.00283739	2.1123
NM_175274 // Ttyh3 // tweety homolog 3 (Drosophila) // 5 G2|5 // 78339 /// XM_006504768	Ttyh3	5.00E-05	2.11259
NM_028014 // 2310067B10Rik // RIKEN cDNA 2310067B10 gene // 11 E2|11 // 71947 /// XM_00	2310067B10Rik	0.00101779	2.11295
NM_010167 // Eya4 // eyes absent 4 homolog (Drosophila) // 10 A3|10 10.44 cM // 14051 /	Eya4	0.0001909	2.1133
NM_001252472 // Cd84 // CD84 antigen // 1 H3|1 79.54 cM // 12523 /// NM_001289470 // Cd	Cd84	1.10E-09	2.1142
NM_009687 // Apex1 // apurinic/apyrimidinic endonuclease 1 // 14 C3|14 26.3 cM // 11792	Apex1	0.000457217	2.11566
NM_028404 // Top1mt // DNA topoisomerase 1, mitochondrial // 15|15 E1 // 72960 /// XR_3	Top1mt	0.000780064	2.11636
NM_011895 // Slc35a1 // solute carrier family 35 (CMP-sialic acid transporter), member	Slc35a1	8.22E-05	2.11678
NM_001033490 // Pusl1 // pseudouridylate synthase-like 1 // 4 E2|4 87.66 cM // 433813 /	Pusl1	0.000591933	2.1169
NM_001252494 // Rapgef6 // Rap guanine nucleotide exchange factor (GEF) 6 // 11 B1.3|11	Rapgef6	0.000167563	2.11694
NM_023045 // Xpo7 // exportin 7 // 14 D2|14 // 65246 /// ENSMUST00000022696 // Xpo7 //	Xpo7	2.86E-06	2.11775
NM_001099349 // Gm14308 // predicted gene 14308 // 2 H4|2 // 100043381 /// NM_001100415	Gm14308	9.97E-08	2.11811
NM_001099349 // Gm14308 // predicted gene 14308 // 2 H4|2 // 100043381 /// NM_001100415	Gm14308	9.97E-08	2.11811
NM_001290376 // Camk1d // calcium/calmodulin-dependent protein kinase ID // 2 A1|2 // 2	Camk1d	1.50E-05	2.11841
NM_008564 // Mcm2 // minichromosome maintenance deficient 2 mitotin (S. cerevisiae) //	Mcm2	0.00155687	2.11973
ENSMUST00000081879 // St6galnac6 // ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-	St6galnac6	0.00238953	2.11979
NM_022980 // Rcan3 // regulator of calcineurin 3 // 4 D3|4 67.59 cM // 53902 /// ENSMUS	Rcan3	0.000128625	2.11989
NM_028015 // Cers5 // ceramide synthase 5 // 15 F1|15 // 71949 /// ENSMUST00000023762 /	Cers5	1.64E-05	2.12197
NM_008323 // Idh3g // isocitrate dehydrogenase 3 (NAD+), gamma // X A7.3-B|X 37.41 cM /	Idh3g	2.70E-07	2.12238
NM_011496 // Aurkb // aurora kinase B // 11 B3|11 42.32 cM // 20877 /// ENSMUST00000021	Aurkb	0.00224147	2.12455
---		0.00387433	2.12612
NM_010832 // Msl3 // male-specific lethal 3 homolog (Drosophila) // X F5|X // 17692 ///	Msl3	0.000316862	2.12732
NM_009761 // Bnip3l // BCL2/adenovirus E1B interacting protein 3-like // 14 D1|14 34.6	Bnip3l	6.75E-07	2.12772
NM_001168541 // Tsku // tsukushi // 7 E2|7 // 244152 /// ENSMUST00000094161 // Tsku //	Tsku	6.44E-06	2.12842
NM_001111311 // Lrrfip1 // leucine rich repeat (in FLII) interacting protein 1 // 1 D|1	Lrrfip1	1.28E-05	2.12896
NM_007624 // Cbx3 // chromobox 3 // 6 B-C|6 24.89 cM // 12417 /// XM_006544713 // LOC10	Cbx3	0.0016918	2.12913
NM_144550 // Spice1 // spindle and centriole associated protein 1 // 16 B4|16 28.67 cM	Spice1	8.57E-05	2.1292
ENSMUST00000031420 // Gpn3 // GPN-loop GTPase 3 // 5 F|5 62.33 cM // 68080 /// ENSMUST0	Gpn3	0.00050402	2.12955
NM_172513 // Fam126b // family with sequence similarity 126, member B // 1 C1.3|1 29.12	Fam126b	1.96E-05	2.12968
NM_013872 // Pmm1 // phosphomannomutase 1 // 15 E1|15 // 29858 /// XM_006521064 // Pmm1	Pmm1	0.000290794	2.13125
AK021184 // Adam10 // a disintegrin and metallopeptidase domain 10 // 9 D|9 39.53 cM //	Adam10	0.00319194	2.13195
AK021184 // Adam10 // a disintegrin and metallopeptidase domain 10 // 9 D|9 39.53 cM //	Adam10	0.00319194	2.13195
NM_145437 // Cd300ld // CD300 molecule-like family member d // 11 E2|11 // 217305 /// E	Cd300ld	4.33E-05	2.13267
NM_001195529 // Gm4980 // predicted gene 4980 // 7 E2|7 // 100503386 /// ENSMUST0000017	Gm4980	0.0029247	2.13349
---		0.00491304	2.13405
NR_040613 // Acss2os // acyl-CoA synthetase short-chain family member 2, opposite stran	Acss2os	0.000526031	2.13553
NR_038162 // Stamos // signal transducing adaptor molecule (SH3 domain and ITAM motif)	Stamos	0.00622194	2.13556
NM_001253812 // Elp3 // elongator acetyltransferase complex subunit 3 // 14 D1|14 // 74	Elp3	2.05E-06	2.13697
NM_001290570 // Ralgps1 // Ral GEF with PH domain and SH3 binding motif 1 // 2 B|2 // 2	Ralgps1	0.000233148	2.13738
ENSMUST00000000199 // Ncs1 // neuronal calcium sensor 1 // 2 B|2 // 14299 /// NM_019681	Ncs1	0.00504038	2.13738
NM_001112711 // Grk6 // G protein-coupled receptor kinase 6 // 13 B1-3|13 30.06 cM // 2	Grk6	0.000131176	2.13771
---		0.00119673	2.13962
NM_001276288 // Aes // amino-terminal enhancer of split // 10 C1|10 39.72 cM // 14797 /	Aes	7.26E-06	2.1399
ENSMUST00000104456 // Gm24982 // predicted gene, 24982 // --- // ---	Gm24982	0.000532037	2.14081
NM_030174 // Mctp1 // multiple C2 domains, transmembrane 1 // 13 C1|13 // 78771 /// ENS	Mctp1	6.23E-05	2.14114
NM_023209 // Pbk // PDZ binding kinase // 14 D1|14 34.36 cM // 52033 /// XM_006519257 /	Pbk	0.000280356	2.14172
NM_145140 // Abcc10 // ATP-binding cassette, sub-family C (CFTR/MRP), member 10 // 17 C	Abcc10	0.00272104	2.14221
NM_029926 // Irak4 // interleukin-1 receptor-associated kinase 4 // 15 F1|15 // 266632	Irak4	8.41E-07	2.14303
NM_001077698 // Fmnl1 // formin-like 1 // 11 D|11 // 57778 /// NM_019679 // Fmnl1 // fo	Fmnl1	6.00E-05	2.14425
XM_006516710 // Zscan26 // zinc finger and SCAN domain containing 26 // 13 A3.1|13 // 4	Zscan26	2.14E-05	2.14514
NM_007415 // Parp1 // poly (ADP-ribose) polymerase family, member 1 // 1 H5|1 84.44 cM	Parp1	1.31E-05	2.14574
NM_001163319 // Tubgcp6 // tubulin, gamma complex associated protein 6 // 15 E3|15 // 3	Tubgcp6	0.00543569	2.14647
NM_021793 // Tmem8 // transmembrane protein 8 (five membrane-spanning domains) // 17|17	Tmem8	1.80E-05	2.14664
NM_001099327 // Gm14305 // predicted gene 14305 // 2 H4|2 // 100043387 /// NM_001099349	Gm14305	1.54E-07	2.14698
NM_172749 // Zfp646 // zinc finger protein 646 // 7 F3|7 // 233905 /// ENSMUST000000503	Zfp646	7.06E-05	2.14779
NM_011734 // Siae // sialic acid acetylesterase // 9 A4|9 20.79 cM // 22619 /// XM_0065	Siae	1.00E-06	2.14821
XR_389000 // LOC102632994 // uncharacterized LOC102632994 // --- // 102632994 /// ENSMU	LOC102632994	0.0052418	2.14825
ENSMUST00000120450 // Gart // phosphoribosylglycinamide formyltransferase // 16 C3-C4|1	Gart	1.62E-05	2.14889
NM_001042541 // Akap1 // A kinase (PRKA) anchor protein 1 // 11 C|11 // 11640 /// NM_00	Akap1	0.000396127	2.14913
NM_029348 // Zbtb4 // zinc finger and BTB domain containing 4 // 11|11 B4 // 75580 ///	Zbtb4	0.00538992	2.14938
NM_134024 // Tubg1 // tubulin, gamma 1 // 11 D|11 64.24 cM // 103733 /// ENSMUST0000004	Tubg1	0.000279669	2.14977
NM_001081107 // Helq // helicase, POLQ-like // 5|5 E // 191578 /// XM_006534827 // Helq	Helq	0.000195987	2.15003
NM_138743 // Smim11 // small integral membrane protein 11 // 16 C4|16 // 68936 // ENSM	Smim11	0.00118299	2.15006
NM_176976 // 5830418K08Rik // RIKEN cDNA 5830418K08 gene // 9 A2|9 // 319675 /// ENSMUS	5830418K08Rik	0.000465295	2.15046
NM_001134829 // Lpgat1 // lysophosphatidylglycerol acyltransferase 1 // 1 H6|1 // 22685	Lpgat1	3.32E-05	2.15142
NM_024288 // Rmnd5a // required for meiotic nuclear division 5 homolog A (S. cerevisiae	Rmnd5a	0.000118481	2.15258
NM_010489 // Hyal2 // hyaluronoglucosaminidase 2 // 9 F1|9 58.12 cM // 15587 /// XM_006	Hyal2	1.51E-06	2.1539
NM_144872 // Eml3 // echinoderm microtubule associated protein like 3 // 19 A|19 // 225	Eml3	0.0005523	2.15552
XR_374487 // Knstrn // kinetochore-localized astrin/SPAG5 binding // 2 E5|2 // 51944 //	Knstrn	0.000173306	2.15621
NM_028354 // Tdp1 // tyrosyl-DNA phosphodiesterase 1 // 12 E|12 // 104884 /// XM_006515	Tdp1	4.91E-07	2.15678
NM_001166642 // Bcas3 // breast carcinoma amplified sequence 3 // 11 C|11 // 192197 ///	Bcas3	2.98E-05	2.15706
NM_025954 // Pgp // phosphoglycolate phosphatase // 17 A3.3|17 // 67078 /// ENSMUST0000	Pgp	0.00409265	2.15812
BC068155 // Plxna2 // plexin A2 // 1 H6|1 // 18845 /// NM_008882 // Plxna2 // plexin A2	Plxna2	4.37E-05	2.15835
NM_198425 // Eid2 // EP300 interacting inhibitor of differentiation 2 // 7 A3|7 // 3866	Eid2	3.82E-05	2.15918
NM_177293 // Mtap7d3 // MAP7 domain containing 3 // X A5|X // 320923 /// XM_006528088 /	Mtap7d3	0.00109856	2.16027
NM_144907 // Sesn2 // sestrin 2 // 4 D2.3|4 // 230784 /// ENSMUST00000030724 // Sesn2 /	Sesn2	0.00504931	2.16087
---		0.00647882	2.16113
NM_181815 // Cep128 // centrosomal protein 128 // 12|12 E // 75216 /// XM_006516326 //	Cep128	5.91E-05	2.16116
NM_001081133 // Kif16b // kinesin family member 16B // 2|2 G3 // 16558 /// XM_006498813	Kif16b	2.48E-06	2.16117
---		0.00358553	2.16179
NM_001177406 // Gm14431 // predicted gene 14431 // 2|2 // 100303732 /// NM_001177407 //	Gm14431	2.16E-08	2.16189
NM_178795 // Ppip5k1 // diphosphoinositol pentakisphosphate kinase 1 // 2 E5|2 // 32765	Ppip5k1	4.15E-05	2.16238
NM_001254761 // Rnf128 // ring finger protein 128 // X F1|X // 66889 /// ENSMUST0000011	Rnf128	4.63E-06	2.16384
NM_025693 // Tmem41a // transmembrane protein 41a // 16 B1|16 // 66664 /// NR_037773 //	Tmem41a	0.000346161	2.16474
XM_006530044 // Gm14434 // predicted gene 14434 // 2 H4|2 // 668039 /// NM_001099349 //	Gm14434	3.07E-07	2.16539
XM_006528794 // Ptchd1 // patched domain containing 1 // X F3|X // 211612 /// NM_001093	Ptchd1	0.000464764	2.16578
ENSMUST00000028294 // Card9 // caspase recruitment domain family, member 9 // 2 A3|2 //	Card9	3.05E-06	2.1663

---		0.000438346	2.16643
NM_010620 // Kif15 // kinesin family member 15 // 9 F4|9 // 209737 /// ENSMUST000000407	Kif15	0.00128576	2.1669
NM_001114660 // Scfd2 // Sec1 family domain containing 2 // 5 C3.3|5 // 212986 /// NM_0	Scfd2	0.000423854	2.16715
NM_172772 // Fam63b // family with sequence similarity 63, member B // 9 D|9 // 235461	Fam63b	1.44E-05	2.16788
NM_001030307 // Dkc1 // dyskeratosis congenita 1, dyskerin // X A7.3|X // 245474 /// EN	Dkc1	0.000305457	2.16814
NR_030716 // 5430417L22Rik // RIKEN cDNA 5430417L22 gene // 2 E5|2 // 100043272 /// ENS	5430417L22Rik	0.000737107	2.16818
NM_026410 // Cdca5 // cell division cycle associated 5 // 19 A|19 // 67849 /// ENSMUST0	Cdca5	0.000200262	2.16828
ENSMUST00000081455 // Gm6917 // predicted gene 6917 // 13 B3|13 // 628794 /// ENSMUST00	Gm6917	3.47E-06	2.16946
ENSMUST00000158426 // Gm23354 // predicted gene, 23354 // --- // ---	Gm23354	0.00556143	2.16997
NM_146234 // Mmgt1 // membrane magnesium transporter 1 // X A5|X // 236792 /// ENSMUST0	Mmgt1	8.70E-05	2.17038
NM_199199 // Tmem199 // transmembrane protein 199 // 11 B5|11 // 195040 /// ENSMUST0000	Tmem199	0.00578899	2.17049
NM_001165980 // Dcaf17 // DDB1 and CUL4 associated factor 17 // 2 C2|2 // 75763 /// NM_	Dcaf17	2.25E-05	2.17051
XM_006511191 // Zbtb38 // zinc finger and BTB domain containing 38 // 9 E3.3|9 // 24500	Zbtb38	0.00010485	2.1718
NM_001163609 // Psma8 // proteasome (prosome, macropain) subunit, alpha type, 8 // 18|1	Psma8	0.0063109	2.17183
NM_001177406 // Gm14431 // predicted gene 14431 // 2|2 // 100303732 /// NM_001177407 //	Gm14431	1.86E-06	2.1722
NM_001177406 // Gm14431 // predicted gene 14431 // 2|2 // 100303732 /// NM_001177407 //	Gm14431	1.86E-06	2.1722
ENSMUST00000141541 // Gm15503 // predicted gene 15503 // --- // --- /// XM_006508140 //	Gm15503	0.000462012	2.17563
NM_026420 // Paip2 // polyadenylate-binding protein-interacting protein 2 // 18 B2|18 /	Paip2	0.000170774	2.17632
NM_001199431 // Dnmt1 // DNA methyltransferase (cytosine-5) 1 // 9 A3|9 7.66 cM // 1343	Dnmt1	4.18E-05	2.17713
NM_001271434 // Haghl // hydroxyacylglutathione hydrolase-like // 17 A3.3|17 // 68977 /	Haghl	4.09E-06	2.17925
NM_001113351 // Synj2 // synaptojanin 2 // 17 A2-A3.1|17 3.59 cM // 20975 /// NM_001113	Synj2	2.59E-06	2.17968
NM_019403 // Rnf5 // ring finger protein 5 // 17 B1|17 18.18 cM // 54197 /// ENSMUST000	Rnf5	0.000249232	2.18221
NM_181547 // Nostrin // nitric oxide synthase trafficker // 2 C2|2 // 329416 /// ENSMUS	Nostrin	5.11E-06	2.18251
NM_001123367 // Gm3448 // predicted gene 3448 // 17 A2|17 // 100041639 /// NM_001123368	Gm3448	0.000327416	2.18325
ENSMUST00000157182 // Gm25559 // predicted gene, 25559 // --- // ---	Gm25559	0.000946094	2.18368
NM_134081 // Dnajc9 // DnaJ (Hsp40) homolog, subfamily C, member 9 // 14 A3|14 // 10867	Dnajc9	0.000203578	2.18397
NM_008857 // Prkci // protein kinase C, iota // 3 A3|3 14.65 cM // 18759 /// ENSMUST000	Prkci	8.52E-05	2.18444
NM_019730 // Nme3 // NME/NM23 nucleoside diphosphate kinase 3 // 17 A3.3|17 // 79059 //	Nme3	0.000405222	2.18522
NM_001024806 // Cebpz // CCAAT/enhancer binding protein zeta // 17 E3|17 // 12607 /// E	Cebpz	8.12E-05	2.18535
NM_015830 // Capn15 // calpain 15 // 17|17 A3 // 50817 /// XM_006524609 // Capn15 // ca	Capn15	3.79E-05	2.18573
NM_001102436 // Acbd5 // acyl-Coenzyme A binding domain containing 5 // 2 A3|2 // 74159	Acbd5	0.00010379	2.18591
NM_001205095 // Gm4944 // predicted gene 4944 // 17 A3.3|17 // 240038 /// XM_006524228	Gm4944	0.00168223	2.18598
NM_177909 // Slc9a9 // solute carrier family 9 (sodium/hydrogen exchanger), member 9 //	Slc9a9	0.000214669	2.18793
NM_134158 // AF251705 // cDNA sequence AF251705 // 11 E2|11 80.57 cM // 140497 /// ENSM	AF251705	0.000354116	2.1883
NM_134021 // Pnpo // pyridoxine 5-phosphate oxidase // 11 D|11 // 103711 /// ENSMUST000	Pnpo	0.000451702	2.18992
NM_013909 // Fbxl6 // F-box and leucine-rich repeat protein 6 // 15 D3|15 // 30840 ///	Fbxl6	0.000565449	2.19062
NR_051998 // Ankzf1 // ankyrin repeat and zinc finger domain containing 1 // 1 C3|1 38.	Ankzf1	0.0014877	2.19101
NM_011623 // Top2a // topoisomerase (DNA) II alpha // 11 D|11 62.91 cM // 21973 /// ENS	Top2a	2.56E-05	2.19166
NM_025939 // Paics // phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribo	Paics	1.84E-05	2.19177
NM_001205336 // Arap3 // ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3 // 1	Arap3	0.00313628	2.1933
NM_024290 // Tnfrsf23 // tumor necrosis factor receptor superfamily, member 23 // 7 F5|	Tnfrsf23	0.00400155	2.19399
NM_001033321 // Tmem231 // transmembrane protein 231 // 8 E1|8 // 234740 /// ENSMUST000	Tmem231	0.00271585	2.19446
NM_025339 // Tmem42 // transmembrane protein 42 // 9 F4|9 73.52 cM // 66079 /// XM_0065	Tmem42	0.00578708	2.19518
NM_011729 // Ercc5 // excision repair cross-complementing rodent repair deficiency, com	Ercc5	0.00111937	2.19554
NM_001039239 // Zfp808 // zinc finger protein 80 // 13 B3|13 // 630579 /// ENSMUST00000	Zfp808	3.51E-05	2.19684
NM_178632 // Ints7 // integrator complex subunit 7 // 1 H6|1 // 77065 /// ENSMUST000000	Ints7	1.43E-07	2.19779
ENSMUST00000056508 // Clcn3 // chloride channel 3 // 8 B3.1|8 30.9 cM // 12725 /// NM_0	Clcn3	0.00162925	2.19781
NM_026276 // Aasdhppt // aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl tr	Aasdhppt	9.60E-05	2.19939
NM_030729 // Nckipsd // NCK interacting protein with SH3 domain // 9 F2|9 // 80987 ///	Nckipsd	5.70E-05	2.19958
XM_006506390 // Atf7ip // activating transcription factor 7 interacting protein // 6 G1	Atf7ip	0.00379499	2.19967
NM_001081163 // Chsy1 // chondroitin sulfate synthase 1 // 7 C|7 // 269941 /// ENSMUST0	Chsy1	0.000342431	2.19967
NM_001286663 // Ssbp1 // single-stranded DNA binding protein 1 // 6|6 B2 // 381760 ///	Ssbp1	0.000269499	2.19996
---		0.00495451	2.20168
NM_177699 // Fhod1 // formin homology 2 domain containing 1 // 8 D3|8 // 234686 /// ENS	Fhod1	1.27E-05	2.20226
NM_001276321 // Cyhr1 // cysteine and histidine rich 1 // 15|15 E1 // 54151 /// NM_0012	Cyhr1	6.27E-06	2.2024
ENSMUST00000148217 // Gm15156 // predicted gene 15156 // --- // ---	Gm15156	0.000182691	2.20256
---		0.000139825	2.20332
NM_028189 // B3gnt3 // UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3 //	B3gnt3	0.000222206	2.20384
NM_207245 // Zfp870 // zinc finger protein 870 // 17 B1|17 // 240066 /// XM_006524252 /	Zfp870	0.00476602	2.20396
NM_153555 // Dcaf8 // DDB1 and CUL4 associated factor 8 // 1 H3|1 79.54 cM // 98193 ///	Dcaf8	5.14E-06	2.20411
NM_001013379 // Zfp930 // zinc finger protein 930 // 8 B3.3|8 // 234358	Zfp930	0.00101409	2.2043
NM_030026 // Mccc2 // methylcrotonoyl-Coenzyme A carboxylase 2 (beta) // 13 D1|13 // 78	Mccc2	0.000509551	2.20446
NM_152814 // Zfp566 // zinc finger protein 566 // 7 B1|7 // 72556 /// ENSMUST0000008878	Zfp566	0.00476481	2.20529
NM_001160399 // Ccdc112 // coiled-coil domain containing 112 // 18 C|18 // 240261 /// E	Ccdc112	0.000350302	2.20631
---		0.00050465	2.20714
NM_172824 // Ccdc14 // coiled-coil domain containing 14 // 16 B3|16 // 239839 /// XM_00	Ccdc14	0.00391292	2.20811
NM_026585 // Fam21 // family with sequence similarity 21 // 6 F1|6 53.76 cM // 28006 //	Fam21	1.03E-06	2.2083
NR_029440 // 2010320M18Rik // RIKEN cDNA 2010320M18 gene // 8|8 // 72093 /// BC051496 /	2010320M18Ri	0.00450527	2.20865
NM_011923 // Angptl2 // angiopoietin-like 2 // 2 B|2 // 26360 /// ENSMUST00000004208 //	Angptl2	2.26E-07	2.20869
NM_028355 // Ndc1 // NDC1 transmembrane nucleoporin // 4 C7|4 // 72787 /// XM_006503423	Ndc1	1.19E-07	2.21024
NM_009592 // Abcb7 // ATP-binding cassette, sub-family B (MDR/TAP), member 7 // X C-D|X	Abcb7	8.73E-06	2.21064
NM_144818 // Ncaph // non-SMC condensin I complex, subunit H // 2 F1|2 // 215387 /// EN	Ncaph	0.00051106	2.21307
NR_030738 // 2410006H16Rik // RIKEN cDNA 2410006H16 gene // 11 B2|11 // 69221 /// ENSMU	2410006H16Rik	0.000178403	2.21331
NM_207225 // Hdac4 // histone deacetylase 4 // 1 D|1 // 208727 /// XM_006529302 // Hdac	Hdac4	0.000536819	2.21382
NM_030697 // Kank3 // KN motif and ankyrin repeat domains 3 // 17 B1|17 17.98 cM // 808	Kank3	0.000272749	2.21404
NM_023431 // Mum1 // melanoma associated antigen (mutated) 1 // 10 C1|10 // 68114 /// X	Mum1	0.000501448	2.2145
NM_173011 // Idh2 // isocitrate dehydrogenase 2 (NADP+), mitochondrial // 7 D3|7 45.43	Idh2	4.63E-08	2.21564
NM_007379 // Abca2 // ATP-binding cassette, sub-family A (ABC1), member 2 // 2 A2-B|2 1	Abca2	9.07E-07	2.21641
NM_178641 // Inpp5f // inositol polyphosphate-5-phosphatase F // 7 F3|7 // 101490 /// E	Inpp5f	0.000492964	2.21642
NM_172580 // Acot6 // acyl-CoA thioesterase 6 // 12 D1|12 // 217700 /// ENSMUST00000056	Acot6	0.000848844	2.2169
NM_001037725 // Fam117b // family with sequence similarity 117, member B // 1 C2|1 // 7	Fam117b	5.64E-06	2.21735
---		0.00665696	2.21754
---		0.00362506	2.21811
NM_029992 // Tchp // trichoplein, keratin filament binding // 5 F|5 // 77832 /// ENSMUS	Tchp	1.96E-05	2.21926
NM_001113408 // Ldb1 // LIM domain binding 1 // 19 C3|19 38.75 cM // 16825 /// NM_01069	Ldb1	1.07E-08	2.21999
NM_178605 // Nop16 // NOP16 nucleolar protein // 13 B1|13 28.83 cM // 28126 /// ENSMUST	Nop16	0.00105787	2.2203
ENSMUST00000097466 // Gm10521 // predicted gene 10521 // --- // 100038548 /// AK143847	Gm10521	0.00195344	2.22146
NM_178652 // Supt3 // suppressor of Ty 3 // 17 B3|17 // 109115 /// XM_006523474 // Supt	Supt3	9.61E-05	2.22168
NM_001291105 // E2f1 // E2F transcription factor 1 // 2 H1|2 76.79 cM // 13555 /// NM_0	E2f1	0.000437263	2.22186

---		0.00583275	2.22284
NM_001081151 // Gan // giant axonal neuropathy // 8 E1|8 // 209239 /// ENSMUST000000644	Gan	0.000742961	2.22364
---		0.000105681	2.22526
NM_144500 // Osbpl2 // oxysterol binding protein-like 2 // 2 H4|2 // 228983 /// ENSMUST	Osbpl2	3.24E-08	2.22571
NM_146106 // Lyplal1 // lysophospholipase-like 1 // 1 H5|1 // 226791 /// ENSMUST0000004	Lyplal1	9.39E-05	2.22776
XM_006504522 // Wbscr27 // Williams Beuren syndrome chromosome region 27 (human) // 5 G	Wbscr27	0.000913608	2.22789
NM_146261 // Fam199x // family with sequence similarity 199, X-linked // X F1|X // 2456	Fam199x	0.000111569	2.2287
NM_016683 // Zkscan5 // zinc finger with KRAB and SCAN domains 5 // 5 G2|5 // 22757 ///	Zkscan5	0.000176709	2.22872
NM_033270 // E2f6 // E2F transcription factor 6 // 12 A1.1|12 8.04 cM // 50496 /// NR_0	E2f6	2.26E-05	2.22886
---		0.0061704	2.22923
NM_008898 // Por // P450 (cytochrome) oxidoreductase // 5 G2|5 75.34 cM // 18984 /// XM	Por	1.89E-06	2.22933
ENSMUST00000023262 // Gm9747 // predicted gene 9747 // --- // --- /// AY169784 // Irs1	Gm9747	6.83E-05	2.22959
---		0.00521277	2.22967
NM_027117 // Klhdc2 // kelch domain containing 2 // 12 C3|12 28.77 cM // 69554 /// ENSM	Klhdc2	1.35E-06	2.23199
NM_008537 // Amacr // alpha-methylacyl-CoA racemase // 15|15 B1 // 17117 /// ENSMUST000	Amacr	0.0025185	2.23207
NR_039562 // Mir5103 // microRNA 5103 // 1|1 13.22 cM // 100628580 /// ENSMUST000001751	Mir5103	1.59E-05	2.23291
---		0.00608848	2.23365
NM_144942 // Csad // cysteine sulfinic acid decarboxylase // 15 F3|15 // 246277 /// XM_	Csad	9.38E-05	2.23503
XM_006515014 // Prkar2b // protein kinase, cAMP dependent regulatory, type II beta // 1	Prkar2b	1.62E-05	2.23581
NM_025931 // Ift27 // intraflagellar transport 27 // 15|15 E2 // 67042 /// ENSMUST00000	Ift27	0.00139825	2.23637
NM_146089 // Haus1 // HAUS augmin-like complex, subunit 1 // 18 E3|18 // 225745 /// XM_	Haus1	0.000164271	2.23693
NM_001039185 // Ceacam1 // carcinoembryonic antigen-related cell adhesion molecule 1 //	Ceacam1	0.000233652	2.23713
NM_026005 // 2610301B20Rik // RIKEN cDNA 2610301B20 gene // 4 A1|4 // 67157 /// ENSMUST	2610301B20Rik	0.00108547	2.23766
NM_010692 // Lbx2 // ladybird homeobox homolog 2 (Drosophila) // 6 C3|6 35.94 cM // 168	Lbx2	0.00016987	2.23937
NM_011505 // Stxbp4 // syntaxin binding protein 4 // 11|11 C // 20913 /// XM_006532736	Stxbp4	0.000180973	2.23971
---		0.0015763	2.24038
ENSMUST00000109020 // Gm14440 // predicted gene 14440 // 2|2 // 100503353 /// ENSMUST00	Gm14440	9.78E-07	2.2411
NM_199446 // Phkb // phosphorylase kinase beta // 8 C3|8 41.61 cM // 102093 /// ENSMUST	Phkb	2.61E-05	2.24127
NM_016756 // Cdk2 // cyclin-dependent kinase 2 // 10 D3|10 // 12566 /// NM_183417 // Cd	Cdk2	2.55E-05	2.24247
NM_011121 // Plk1 // polo-like kinase 1 // 7 F3|7 65.52 cM // 18817 /// ENSMUST00000033	Plk1	7.55E-05	2.24465
NM_001177406 // Gm14431 // predicted gene 14431 // 2|2 // 100303732 /// NM_001177407 //	Gm14431	1.18E-06	2.24639
NM_025914 // Actr6 // ARP6 actin-related protein 6 // 10 C2|10 // 67019 /// XM_00651396	Actr6	0.00324858	2.24656
NM_172437 // Pus7l // pseudouridylate synthase 7 homolog (S. cerevisiae)-like // 15 E3|	Pus7l	6.51E-05	2.24709
NM_001289522 // Cad // carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, an	Cad	4.72E-05	2.24733
NM_145128 // Mgat5 // mannoside acetylglucosaminyltransferase 5 // 1 E3|1 // 107895 ///	Mgat5	0.00205729	2.24777
NM_001290986 // Wdr76 // WD repeat domain 76 // 2|2 F1 // 241627 /// NM_001290987 // Wd	Wdr76	8.57E-05	2.2488
NM_009104 // Rrm2 // ribonucleotide reductase M2 // 12 A1.3|12 8.5 cM // 20135 /// ENSM	Rrm2	9.88E-07	2.25182
NM_022331 // Herpud1 // homocysteine-inducible, endoplasmic reticulum stress-inducible,	Herpud1	7.97E-07	2.25308
NM_001163527 // Itpripl1 // inositol 1,4,5-triphosphate receptor interacting protein-li	Itpripl1	2.88E-06	2.25314
NM_001244692 // St18 // suppression of tumorigenicity 18 // 1 A1|1 // 240690 /// NM_001	St18	4.65E-07	2.25427
NM_001164362 // Cep55 // centrosomal protein 55 // 19|19 C3 // 74107 /// NM_028293 // C	Cep55	0.00227243	2.25454
---		0.000305216	2.25563
NM_027891 // Lrwd1 // leucine-rich repeats and WD repeat domain containing 1 // 5 G2|5	Lrwd1	7.93E-05	2.25652
NM_177036 // Ceacam19 // carcinoembryonic antigen-related cell adhesion molecule 19 //	Ceacam19	0.000543992	2.25672
NM_001109688 // C2cd5 // C2 calcium-dependent domain containing 5 // 6|6 G2 // 74741 //	C2cd5	0.000105078	2.25881
NR_045008 // Gm20300 // predicted gene, 20300 // 10|10 17.1 cM // 100504586	Gm20300	0.00145244	2.25893
NM_009968 // Cryz // crystallin, zeta // 3 H4|3 // 12972 /// XM_006500973 // Cryz // cr	Cryz	8.49E-05	2.2607
NM_001113478 // Frrs1 // ferric-chelate reductase 1 // 3 G1|3 // 20321 /// NM_009146 //	Frrs1	1.80E-08	2.26191
ENSMUST00000067888 // Tpk1 // thiamine pyrophosphokinase // 6|6 B2 // 29807 /// NM_0138	Tpk1	0.00048912	2.26207
NM_001111062 // Comt // catechol-O-methyltransferase // 16 A3|16 11.4 cM // 12846 /// N	Comt	1.13E-05	2.26266
NM_001253717 // Atg7 // autophagy related 7 // 6 E3|6 // 74244 /// NM_001253718 // Atg7	Atg7	2.74E-08	2.26323
NM_011849 // Nek4 // NIMA (never in mitosis gene a)-related expressed kinase 4 // 14 B|	Nek4	0.00126456	2.2635
NM_178778 // Scai // suppressor of cancer cell invasion // 2 B|2 // 320271 /// ENSMUST0	Scai	3.46E-05	2.26379
NM_008181 // Gsta1 // glutathione S-transferase, alpha 1 (Ya) // 9 E1|9 43.65 cM // 148	Gsta1	0.00481631	2.26492
NM_026810 // Mlh1 // mutL homolog 1 (E. coli) // 9 F3|9 60.92 cM // 17350 /// XM_006511	Mlh1	0.000164756	2.26514
ENSMUST00000140566 // Xxylt1 // xyloside xylosyltransferase 1 // 16 B2|16 // 268880 ///	Xxylt1	0.000357804	2.26524
ENSMUST00000057844 // B230219D22Rik // RIKEN cDNA B230219D22 gene // 13 B1|13 // 78521	B230219D22Rik	2.88E-07	2.26554
NM_001167914 // Atxn3 // ataxin 3 // 12 E|12 // 110616 /// NM_029705 // Atxn3 // ataxin	Atxn3	1.91E-05	2.26597
NM_001081423 // Ttll5 // tubulin tyrosine ligase-like family, member 5 // 12|12 D3 // 3	Ttll5	0.000198579	2.26806
NM_007422 // Adss // adenylosuccinate synthetase, non muscle // 1 H4|1 // 11566 /// XM_	Adss	1.80E-06	2.26896
NR_015543 // 2810055G20Rik // RIKEN cDNA 2810055G20 gene // 16 C3.1|16 // 77994 /// ENS	2810055G20Rik	0.00491562	2.26921
NM_025835 // Pccb // propionyl Coenzyme A carboxylase, beta polypeptide // 9 E4|9 // 66	Pccb	0.00188918	2.27037
NM_008650 // Mut // methylmalonyl-Coenzyme A mutase // 17 C-D|17 19.55 cM // 17850 ///	Mut	5.21E-06	2.27057
XR_396594 // LOC102638208 // uncharacterized LOC102638208 // --- // 102638208 /// ENSMU	LOC102638208	0.00287808	2.27074
NM_001163643 // Map3k12 // mitogen-activated protein kinase kinase kinase 12 // 15 F3|1	Map3k12	0.000773391	2.27398
NM_080446 // Helb // helicase (DNA) B // 10 D2|10 67.94 cM // 117599 /// ENSMUST0000002	Helb	5.16E-05	2.27445
NM_172692 // Gba2 // glucosidase beta 2 // 4 B1|4 // 230101 /// ENSMUST00000030189 // G	Gba2	8.60E-07	2.27532
NM_009471 // Umps // uridine monophosphate synthetase // 16 B3|16 // 22247 /// XM_00652	Umps	7.67E-05	2.27596
NR_015572 // 1810014B01Rik // RIKEN cDNA 1810014B01 gene // 10|10 // 66263 /// ENSMUST0	1810014B01Rik	3.60E-05	2.28224
NM_001085522 // Gm13251 // predicted gene 13251 // 4 E1|4 // 433791 /// ENSMUST00000105	Gm13251	0.000536732	2.28365
NM_001290805 // Kif3a // kinesin family member 3A // 11 A5-B1|11 31.97 cM // 16568 ///	Kif3a	1.28E-06	2.28391
NM_028846 // Usp20 // ubiquitin specific peptidase 20 // 2 B|2 // 74270 /// XM_00649839	Usp20	0.000258428	2.28392
NM_173047 // Cbr3 // carbonyl reductase 3 // 16 C4|16 54.58 cM // 109857 /// ENSMUST000	Cbr3	0.00146809	2.28395
NM_001081158 // Cluh // clustered mitochondria (cluA/CLU1) homolog // 11 B4|11 // 74148	Cluh	6.62E-06	2.28398
NR_045872 // Gm9054 // predicted gene 9054 // 3 F2.1|3 // 668224	Gm9054	0.000395323	2.2843
NM_001082485 // Zfp266 // zinc finger protein 266 // 9 A3|9 // 77519 /// NM_001135019 /	Zfp266	4.36E-06	2.28495
NM_173400 // Haus6 // HAUS augmin-like complex, subunit 6 // 4 C4|4 40.69 cM // 230376	Haus6	0.00655314	2.28586
NM_027903 // Dhdh // dihydrodiol dehydrogenase (dimeric) // 7 B2|7 29.32 cM // 71755 //	Dhdh	2.51E-07	2.28611
NM_172405 // Fam175a // family with sequence similarity 175, member A // 5 E4|5 // 7068	Fam175a	2.71E-06	2.28743
NM_027185 // Def6 // differentially expressed in FDCP 6 // 17 A3.3|17 // 23853 /// ENSM	Def6	0.00178009	2.28916
NM_008512 // Lrp1 // low density lipoprotein receptor-related protein 1 // 10|10 B2-D1	Lrp1	9.87E-05	2.28942
NM_134420 // Slc26a6 // solute carrier family 26, member 6 // 9 F2|9 // 171429 /// ENSM	Slc26a6	2.31E-06	2.29087
---		0.00112324	2.29121
XR_387513 // 6230416C02Rik // RIKEN cDNA 6230416C02 gene // 2 H4|2 // 545490 /// NM_001	6230416C02Rik	2.00E-07	2.29133
NM_007988 // Fasn // fatty acid synthase // 11 E2|11 84.56 cM // 14104 /// ENSMUST00000	Fasn	6.13E-07	2.29201
NM_018869 // Grk5 // G protein-coupled receptor kinase 5 // 19 D3|19 56.52 cM // 14773	Grk5	8.15E-05	2.29278
NM_053119 // Echs1 // enoyl Coenzyme A hydratase, short chain, 1, mitochondrial // 7 F4	Echs1	2.11E-05	2.29284
ENSMUST00000139492 // Gm13710 // predicted gene 13710 // 2 D|2 // 672763	Gm13710	0.00256092	2.29337
NM_001165253 // Ctage5 // CTAGE family, member 5 // 12 C1|12 26.01 cM // 217615 /// NM_	Ctage5	1.73E-06	2.29345

NM_028820 // 1700017B05Rik // RIKEN cDNA 1700017B05 gene // 9 C|9 30.89 cM // 74211 ///	1700017B05Rik	7.95E-05	2.29361
NM_019484 // Alyref2 // Aly/REF export factor 2 // 1 H3|1 // 56009 /// ENSMUST000000815	Alyref2	0.00232703	2.29367
---		4.36E-05	2.29372
ENSMUST00000014892 // Tex261 // testis expressed gene 261 // 6 C3|6 35.94 cM // 21766 /	Tex261	1.96E-05	2.29376
NM_145928 // Tspan14 // tetraspanin 14 // 14 B|14 22.36 cM // 52588 /// XM_006519261 //	Tspan14	2.05E-05	2.29629
NM_010441 // Hmga2 // high mobility group AT-hook 2 // 10 D2|10 67.94 cM // 15364 /// E	Hmga2	0.000474527	2.29662
NM_029631 // Abhd14b // abhydrolase domain containing 14b // 9 F1|9 // 76491 /// XM_006	Abhd14b	0.000620664	2.29871
NM_001033294 // Ddx31 // DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31 // 2 A3|2 // 2	Ddx31	0.00155558	2.3028
NM_138587 // Fam3c // family with sequence similarity 3, member C // 6 A3.1|6 9.24 cM /	Fam3c	1.56E-05	2.30303
NM_001159369 // Polq // polymerase (DNA directed), theta // 16 B3|16 26.32 cM // 77782	Polq	0.000145124	2.30394
ENSMUST00000180820 // C630016N16Rik // RIKEN cDNA C630016N16 gene // 7 B1|7 // 791088 /	C630016N16Ril	0.000112169	2.30492
---		0.000102613	2.30533
NM_001163073 // Lcorl // ligand dependent nuclear receptor corepressor-like // 5 B3|5 /	Lcorl	4.76E-06	2.30645
NM_001290662 // Kif2c // kinesin family member 2C // 4 D1|4 53.42 cM // 73804 /// NM_13	Kif2c	7.19E-05	2.30651
NM_011948 // Map3k4 // mitogen-activated protein kinase kinase kinase 4 // 17 A1|17 8.4	Map3k4	3.43E-05	2.30714
NM_178798 // Slc7a6 // solute carrier family 7 (cationic amino acid transporter, y+ sys	Slc7a6	1.65E-06	2.3077
NM_147220 // Abca9 // ATP-binding cassette, sub-family A (ABC1), member 9 // 11 E1|11 /	Abca9	1.54E-05	2.30829
NM_198292 // Tex2 // testis expressed gene 2 // 11 D|11 69.46 cM // 21763 /// XM_006533	Tex2	2.04E-05	2.30853
NM_001081189 // Uprt // uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	Uprt	4.28E-06	2.30888
NM_011391 // Slc16a7 // solute carrier family 16 (monocarboxylic acid transporters), me	Slc16a7	1.26E-06	2.31025
NM_001081353 // 2210408I21Rik // RIKEN cDNA 2210408I21 gene // 13 C1|13 // 72371 /// NM	2210408I21Rik	4.08E-05	2.31032
NM_139303 // Kif18a // kinesin family member 18A // 2 E3|2 // 228421 /// ENSMUST0000002	Kif18a	0.00253734	2.31148
NM_001081098 // Zfp362 // zinc finger protein 362 // 4 D2.2|4 // 230761 /// ENSMUST0000	Zfp362	7.31E-06	2.31203
---		1.73E-05	2.31336
NM_176979 // Topbp1 // topoisomerase (DNA) II binding protein 1 // 9 F1|9 // 235559 ///	Topbp1	2.23E-05	2.31381
ENSMUST00000109020 // Gm14440 // predicted gene 14440 // 2|2 // 100503353 /// ENSMUST00	Gm14440	7.80E-08	2.31435
NM_175360 // Obfc1 // oligonucleotide/oligosaccharide-binding fold containing 1 // 19 D	Obfc1	1.45E-05	2.31551
NM_029249 // Parpbp // PARP1 binding protein // 10 C2|10 // 75317 /// ENSMUST0000004851	Parpbp	0.00166508	2.31611
NM_023737 // Ehhadh // enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogena	Ehhadh	0.000196923	2.31705
NM_080795 // Lnx2 // ligand of numb-protein X 2 // 5|5 G2 // 140887 /// ENSMUST00000016	Lnx2	9.94E-05	2.32117
NM_173450 // Rpusd2 // RNA pseudouridylate synthase domain containing 2 // 2 E5|2 // 27	Rpusd2	2.84E-05	2.32134
ENSMUST00000180951 // D130017N08Rik // RIKEN cDNA D130017N08 gene // 5 G2|5 // 320064 /	D130017N08Ril	5.66E-05	2.32259
XR_387077 // Ap1s2 // adaptor-related protein complex 1, sigma 2 subunit // X F5|X // 1	Ap1s2	1.88E-06	2.32308
NM_080462 // Hnmt // histamine N-methyltransferase // 2 A3|2 // 140483 /// XM_006497671	Hnmt	6.89E-05	2.32459
NM_199447 // Rrp12 // ribosomal RNA processing 12 homolog (S. cerevisiae) // 19 C3|19 /	Rrp12	0.000151591	2.32462
NM_019665 // Arl6 // ADP-ribosylation factor-like 6 // 16|16 C1.2 // 56297 /// ENSMUST0	Arl6	6.56E-05	2.32651
NM_009730 // Atrn // attractin // 2 F1|2 63.26 cM // 11990 /// ENSMUST00000028781 // At	Atrn	1.80E-06	2.32683
NM_001111017 // Serac1 // serine active site containing 1 // 17 A1|17 3.67 cM // 321007	Serac1	8.76E-07	2.32761
NM_001122989 // Cdc14b // CDC14 cell division cycle 14B // 13 B3|13 // 218294 /// NM_17	Cdc14b	0.000104877	2.3279
NM_174848 // Crybg3 // beta-gamma crystallin domain containing 3 // 16 C1.3|16 // 22427	Crybg3	1.30E-06	2.32883
NM_027895 // Ulk3 // unc-51-like kinase 3 // 9|9 C // 71742 /// XR_379456 // Ulk3 // un	Ulk3	0.00357633	2.32964
NM_001127351 // Sirt3 // sirtuin 3 // 7|7 F4 // 64384 /// NM_001177804 // Sirt3 // sirt	Sirt3	0.00270536	2.33062
NM_025522 // Dhrs7 // dehydrogenase/reductase (SDR family) member 7 // 12 C3|12 // 6637	Dhrs7	4.73E-06	2.33159
NM_001013256 // Ctc1 // CTS telomere maintenance complex component 1 // 11 B3|11 // 689	Ctc1	1.15E-06	2.33176
NM_011779 // Coro1c // coronin, actin binding protein 1C // 5 F|5 // 23790 /// ENSMUST0	Coro1c	7.84E-08	2.33396
XM_006522459 // Cmss1 // cms small ribosomal subunit 1 // 16 C1.1|16 // 66497 /// XM_00	Cmss1	0.00170036	2.33577
NM_177780 // Dock5 // dedicator of cytokinesis 5 // 14 D1|14 // 68813 /// ENSMUST000000	Dock5	2.66E-07	2.33621
NM_011467 // Spr // sepiapterin reductase // 6 C3|6 37.15 cM // 20751 /// ENSMUST000000	Spr	0.00195049	2.33659
---		0.00104491	2.33702
NM_028335 // Zfp248 // zinc finger protein 248 // 6 F1|6 // 72720 /// XM_006506676 // Z	Zfp248	0.000105512	2.34052
NM_146151 // Tesk2 // testis-specific kinase 2 // 4 D1|4 // 230661 /// ENSMUST000000455	Tesk2	0.00112008	2.34284
ENSMUST00000120593 // Bcl7a // B cell CLL/lymphoma 7A // 5 F|5 // 77045 /// NM_029850 /	Bcl7a	0.000225122	2.34351
NM_001025586 // Nr2c2ap // nuclear receptor 2C2-associated protein // 8 B3.3|8 // 75692	Nr2c2ap	0.00313757	2.34387
NM_009547 // Zbtb14 // zinc finger and BTB domain containing 14 // 17 E1.3|17 40.42 cM	Zbtb14	0.00010163	2.34402
ENSMUST00000180411 // Gm17491 // predicted gene, 17491 // 8|8 11.42 cM // 100502938	Gm17491	2.23E-05	2.34421
NM_001040395 // Nadk2 // NAD kinase 2, mitochondrial // 15|15 A2 // 68646 /// NM_001085	Nadk2	3.34E-05	2.3445
NM_001294322 // Mpv17 // MpV17 mitochondrial inner membrane protein // 5 B1|5 // 17527	Mpv17	7.81E-06	2.34507
---		0.00500611	2.3468
---		0.00500611	2.3468
NM_009560 // Zfp60 // zinc finger protein 60 // 7 A3|7 15.97 cM // 22718 /// ENSMUST000	Zfp60	0.00465339	2.34706
ENSMUST00000181295 // Gm26895 // predicted gene, 26895 // --- // ---	Gm26895	0.000916429	2.34733
NM_028276 // Utp14a // UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast) /	Utp14a	2.21E-07	2.34771
NM_001198785 // Aatk // apoptosis-associated tyrosine kinase // 11 E2|11 // 11302 /// N	Aatk	0.000232864	2.34957
NM_007382 // Acadm // acyl-Coenzyme A dehydrogenase, medium chain // 3 H3|3 78.77 cM //	Acadm	7.84E-07	2.35006
NM_001037955 // Dusp22 // dual specificity phosphatase 22 // 13 A3.2|13 // 105352 /// N	Dusp22	5.56E-07	2.35016
NM_133947 // Numa1 // nuclear mitotic apparatus protein 1 // 7 E3|7 // 101706 /// XM_00	Numa1	1.99E-05	2.35121
NM_198305 // Klhl17 // kelch-like 17 // 4 E2|4 // 231003 /// ENSMUST00000105569 // Klhl	Klhl17	0.000192269	2.35236
NM_173347 // Prune // prune homolog (Drosophila) // 3 F2.1|3 // 229589 /// ENSMUST00000	Prune	1.53E-05	2.35267
NM_153126 // Nat10 // N-acetyltransferase 10 // 2 E2|2 // 98956 /// XM_006500455 // Nat	Nat10	4.12E-05	2.35358
NM_008855 // Prkcb // protein kinase C, beta // 7 F3|7 65.75 cM // 18751 /// ENSMUST000	Prkcb	1.24E-06	2.35358
NM_175158 // Utp20 // UTP20, small subunit (SSU) processome component, homolog (yeast)	Utp20	6.71E-06	2.35402
NM_181417 // Csrp2bp // cysteine and glycine-rich protein 2 binding protein // 2 G1|2 7	Csrp2bp	0.000275039	2.35767
NM_023166 // Fam89b // family with sequence similarity 89, member B // 19 A|19 4.34 cM	Fam89b	3.60E-05	2.36007
ENSMUST00000182761 // Gm20204 // predicted gene, 20204 // --- // ---	Gm20204	0.00132864	2.36031
---		0.00040221	2.36141
NR_002900 // Snora69 // small nucleolar RNA, H/ACA box 69 // X A3.3|X // 104369 /// ENS	Snora69	0.00533264	2.36148
NM_007564 // Zfp36l1 // zinc finger protein 36, C3H type-like 1 // 12 C3|12 // 12192 //	Zfp36l1	2.73E-05	2.3619
ENSMUST00000124845 // Sgsm3 // small G protein signaling modulator 3 // 15 E1|15 // 105	Sgsm3	0.00147725	2.36209
NM_029321 // Ttc32 // tetratricopeptide repeat domain 32 // 12|12 A1.3 // 75516 /// ENS	Ttc32	0.000236685	2.36215
NM_008964 // Ptger2 // prostaglandin E receptor 2 (subtype EP2) // 14 C1|14 22.68 cM //	Ptger2	2.50E-05	2.36313
NM_153104 // Phospho1 // phosphatase, orphan 1 // 11 D|11 59.01 cM // 237928 /// ENSMUS	Phospho1	0.00320414	2.36388
AK144456 // Gm19703 // predicted gene, 19703 // 14|14 22.36 cM // 100503457	Gm19703	0.0064732	2.36518
NM_001289429 // Cipc // CLOCK interacting protein, circadian // 12 D2|12 // 217732 ///	Cipc	6.13E-07	2.36519
ENSMUST00000075558 // Hist2h3b // histone cluster 2, H3b // 3 F2.1|3 // 319154 /// ENSM	Hist2h3b	0.00618477	2.3654
NM_175534 // Mrgpre // MAS-related GPR, member E // 7 F5|7 // 244238 /// ENSMUST0000005	Mrgpre	0.000394503	2.36652
NM_007520 // Bach1 // BTB and CNC homology 1 // 16 C3.3|16 // 12013 /// ENSMUST00000026	Bach1	6.35E-08	2.36717
NM_001205241 // Kat6b // K(lysine) acetyltransferase 6B // 14 A3|14 // 54169 /// NM_017	Kat6b	0.000431291	2.36782
NR_028281 // Snord43 // small nucleolar RNA, C/D box 43 // 15 E1|15 // 100302600	Snord43	0.00552183	2.36849
NM_001170333 // Clec4a2 // C-type lectin domain family 4, member a2 // 6 F3|6 58.18 cM	Clec4a2	0.000272358	2.36893

NM_001113486 // Sept9 // septin 9 // 11 E2|11 82.61 cM // 53860 /// NM_001113488 // Sep	Sep-09	4.32E-08	2.36911
NM_198411 // Inf2 // inverted formin, FH2 and WH2 domain containing // 12 F1|12 // 7043	Inf2	0.000582474	2.36936
---		0.00623899	2.36961
NM_029861 // Cnrip1 // cannabinoid receptor interacting protein 1 // 11|11 A3.1 // 3806	Cnrip1	0.000800361	2.37027
NM_134054 // Sptssa // serine palmitoyltransferase, small subunit A // 12 C1|12 // 1047	Sptssa	0.000782767	2.37034
NM_144558 // Bivm // basic, immunoglobulin-like variable motif containing // 1 C1.1|1 /	Bivm	2.52E-05	2.37073
NM_001271397 // Nol8 // nucleolar protein 8 // 13 B1|13 25.36 cM // 70930 /// NR_073167	Nol8	7.14E-07	2.37104
ENSMUST00000101077 // A530017D24Rik // RIKEN cDNA A530017D24 gene // --- // --- /// ENS	A530017D24Ril	6.88E-05	2.37112
NM_028758 // Gga2 // golgi associated, gamma adaptin ear containing, ARF binding protei	Gga2	1.76E-05	2.37121
NM_009898 // Coro1a // coronin, actin binding protein 1A // 7 F3|7 69.25 cM // 12721 //	Coro1a	4.35E-06	2.37168
NM_001163622 // Prepl // prolyl endopeptidase-like // 17 E4|17 // 213760 /// NM_0011636	Prepl	4.53E-06	2.37244
NM_028761 // Parn // poly(A)-specific ribonuclease (deadenylation nuclease) // 16|16 B1	Parn	0.0017242	2.37254
NM_001024604 // Ankrd28 // ankyrin repeat domain 28 // 14 B|14 // 105522 /// ENSMUST000	Ankrd28	1.37E-05	2.37279
XR_404983 // LOC102635305 // uncharacterized LOC102635305 // --- // 102635305 /// ENSMU	LOC102635305	0.000247763	2.37281
NM_025294 // Natd1 // N-acetyltransferase domain containing 1 // 11 B2|11 // 24083 ///	Natd1	1.76E-05	2.37658
NM_133943 // Hsd3b7 // hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta	Hsd3b7	8.20E-05	2.37796
---		0.00330554	2.37827
NM_026812 // Hddc3 // HD domain containing 3 // 7 D3|7 // 68695 /// ENSMUST00000032747	Hddc3	0.000264677	2.37884
---		0.00132548	2.38109
NM_146108 // Hibch // 3-hydroxyisobutyryl-Coenzyme A hydrolase // 1 C1.1|1 // 227095 //	Hibch	0.000730385	2.38175
NM_010124 // Eif4ebp2 // eukaryotic translation initiation factor 4E binding protein 2	Eif4ebp2	0.000130281	2.38192
NM_152822 // Las1l // LAS1-like (S. cerevisiae) // X C3|X // 76130 /// ENSMUST000000799	Las1l	8.05E-06	2.38193
NM_009228 // Snta1 // syntrophin, acidic 1 // 2 H1|2 76.52 cM // 20648 /// ENSMUST00000	Snta1	8.06E-05	2.38226
NM_030715 // Polh // polymerase (DNA directed), eta (RAD 30 related) // 17|17 C // 8090	Polh	0.00234791	2.38343
NM_001083334 // Bin1 // bridging integrator 1 // 18 B1|18 18.01 cM // 30948 /// NM_0096	Bin1	7.67E-07	2.38403
NM_001177406 // Gm14431 // predicted gene 14431 // 2|2 // 100303732 /// NM_001177407 //	Gm14431	5.48E-07	2.38446
ENSMUST00000122924 // Nudt8 // nudix (nucleoside diphosphate linked moiety X)-type moti	Nudt8	0.00390209	2.38577
NM_021356 // Gab1 // growth factor receptor bound protein 2-associated protein 1 // 8 C	Gab1	7.10E-07	2.38641
NM_021555 // Fam203a // family with sequence similarity 203, member A // 15 D3|15 35.78	Fam203a	0.00271615	2.38745
NM_008795 // Cdk18 // cyclin-dependent kinase 18 // 1 E4|1 // 18557 /// XR_387152 // Cd	Cdk18	7.18E-09	2.38796
NM_001289666 // Tmem241 // transmembrane protein 241 // 18 A1|18 // 338363 /// NM_00128	Tmem241	8.14E-06	2.39084
NM_001081368 // Tbccd1 // TBCC domain containing 1 // 16 B1|16 // 70573 /// XM_00652256	Tbccd1	1.54E-05	2.39091
---		0.00427787	2.39158
NM_027560 // Arrdc2 // arrestin domain containing 2 // 8|8 C1 // 70807 /// ENSMUST00000	Arrdc2	0.000635508	2.39195
NM_182995 // Ccp110 // centriolar coiled coil protein 110 // 7 F2|7 // 101565 /// ENSMU	Ccp110	8.57E-05	2.39256
NM_021392 // Ap4m1 // adaptor-related protein complex AP-4, mu 1 // 5|5 G1 // 11781 ///	Ap4m1	5.31E-06	2.39292
NM_029148 // Tmx4 // thioredoxin-related transmembrane protein 4 // 2 G1|2 65.66 cM //	Tmx4	8.26E-05	2.39439
NM_199033 // Tsen2 // tRNA splicing endonuclease 2 homolog (S. cerevisiae) // 6 E3|6 //	Tsen2	0.00496094	2.39536
NM_023284 // Nuf2 // NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Nuf2	0.000353768	2.39599
NM_178664 // B3gntl1 // UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-lik	B3gntl1	0.000215719	2.39612
NM_153780 // 2610044O15Rik8 // RIKEN cDNA 2610044O15 gene // 8 E2|8 // 72139 /// BC0238	2610044O15Ril	0.00325599	2.39683
NR_030670 // Gm15760 // mitochondrial ribosomal protein S18B pseudogene // 16 A3|16 //	Gm15760	1.45E-05	2.39695
NM_001205236 // Arhgap27 // Rho GTPase activating protein 27 // 11 E1|11 // 544817 ///	Arhgap27	0.000112681	2.4001
NM_001128094 // Atp13a3 // ATPase type 13A3 // 16 B2|16 // 224088 /// NM_001128096 // A	Atp13a3	1.33E-06	2.40094
NM_008017 // Smc2 // structural maintenance of chromosomes 2 // 4 B3|4 28.31 cM // 1421	Smc2	3.65E-05	2.40149
NM_181541 // Caprin2 // caprin family member 2 // 6 G3|6 // 232560 /// ENSMUST000000723	Caprin2	0.000738078	2.4021
AK144475 // Nr2f6 // nuclear receptor subfamily 2, group F, member 6 // 8 B3.3|8 34.43	Nr2f6	0.00263242	2.40252
NM_153560 // Fam102a // family with sequence similarity 102, member A // 2 B|2 // 98952	Fam102a	4.49E-05	2.40261
NM_026174 // Entpd4 // ectonucleoside triphosphate diphosphohydrolase 4 // 14 D2|14 //	Entpd4	2.62E-09	2.40262
NM_175212 // Tmem65 // transmembrane protein 65 // 15 D1|15 // 74868 /// ENSMUST0000007	Tmem65	1.23E-06	2.40313
NM_144815 // Cecr5 // cat eye syndrome chromosome region, candidate 5 // 6 F1|6 56.95 c	Cecr5	0.00126825	2.40316
NM_028792 // Josd1 // Josephin domain containing 1 // 15 E1|15 // 74158 /// XM_00148098	Josd1	3.57E-05	2.40351
NM_177353 // Slc9a7 // solute carrier family 9 (sodium/hydrogen exchanger), member 7 //	Slc9a7	2.98E-05	2.40606
---		0.00606163	2.40697
NM_001145898 // BC052040 // cDNA sequence BC052040 // 2 E4|2 // 399568 /// NM_207264 //	BC052040	0.00130537	2.40739
XM_006534256 // Coasy // Coenzyme A synthase // 11 D|11 // 71743 /// ENSMUST00000001806	Coasy	8.15E-05	2.40791
NM_009211 // Smarcc1 // SWI/SNF related, matrix associated, actin dependent regulator o	Smarcc1	0.000264712	2.40896
NM_019933 // Ptpn4 // protein tyrosine phosphatase, non-receptor type 4 // 1 E2|1 52.39	Ptpn4	3.80E-05	2.40931
NM_019455 // Hpgds // hematopoietic prostaglandin D synthase // 6|6 D-E // 54486 /// EN	Hpgds	7.67E-06	2.41003
NM_019864 // Atr // ataxia telangiectasia and Rad3 related // 9 E4|9 // 245000 /// ENSM	Atr	0.000248518	2.41046
NM_172289 // Slc36a4 // solute carrier family 36 (proton/amino acid symporter), member	Slc36a4	6.18E-06	2.41236
NM_010244 // Fv1 // Friend virus susceptibility 1 // 4 E2|4 78.56 cM // 14349 /// ENSMU	Fv1	0.00296833	2.41275
NM_001163421 // Tatdn3 // TatD DNase domain containing 3 // 1 H6|1 // 68972 /// NM_0011	Tatdn3	1.52E-05	2.41306
NM_001014974 // Ttll4 // tubulin tyrosine ligase-like family, member 4 // 1 C3|1 // 675	Ttll4	0.0020628	2.4133
AK134193 // Gm19313 // predicted gene, 19313 // 4 E2|4 86.17 cM // 100502668	Gm19313	0.000385729	2.4137
NM_013454 // Abca1 // ATP-binding cassette, sub-family A (ABC1), member 1 // 4 A5-B3|4	Abca1	1.00E-09	2.41396
NM_025957 // Ceacam14 // carcinoembryonic antigen-related cell adhesion molecule 14 //	Ceacam14	0.00373775	2.4145
NM_011762 // Zfp59 // zinc finger protein 59 // 7 A3|7 // 22717 /// XM_006539744 // Zfp	Zfp59	1.01E-05	2.41459
NM_025377 // Ska2 // spindle and kinetochore associated complex subunit 2 // 11 C|11 //	Ska2	0.000343914	2.41818
NM_015818 // Hs6st1 // heparan sulfate 6-O-sulfotransferase 1 // 1 B|1 // 50785 /// ENS	Hs6st1	0.000440687	2.42001
NM_145960 // Mtrf1 // mitochondrial translational release factor 1 // 14 D3|14 // 21125	Mtrf1	0.00109378	2.42115
NM_178162 // Agfg2 // ArfGAP with FG repeats 2 // 5 G2|5 // 231801 /// XM_006504567 //	Agfg2	5.19E-06	2.42285
NM_028428 // Fut11 // fucosyltransferase 11 // 14|14 B // 73068 /// ENSMUST00000048016	Fut11	1.24E-06	2.42594
ENSMUST00000131743 // Polr2e // polymerase (RNA) II (DNA directed) polypeptide E // 10	Polr2e	1.23E-06	2.4275
NM_001042527 // Blm // Bloom syndrome, RecQ helicase-like // 7 D3|7 45.65 cM // 12144 /	Blm	8.32E-05	2.42928
NM_181584 // Gab3 // growth factor receptor bound protein 2-associated protein 3 // X A	Gab3	0.000283164	2.4294
NM_010302 // Gna12 // guanine nucleotide binding protein, alpha 12 // 5 G2|5 79.3 cM //	Gna12	4.50E-07	2.42949
NM_172371 // Slc16a13 // solute carrier family 16 (monocarboxylic acid transporters), m	Slc16a13	3.90E-05	2.4327
XR_382919 // LOC102636620 // uncharacterized LOC102636620 // --- // 102636620 /// ENSMU	LOC102636620	0.000337138	2.43277
---		0.0019873	2.43463
ENSMUST00000110934 // Cnpy4 // canopy 4 homolog (zebrafish) // 5 G2|5 // 66455 /// BC09	Cnpy4	2.41E-05	2.43469
NM_026891 // Cdan1 // congenital dyserythropoietic anemia, type I (human) // 2 E5|2 //	Cdan1	1.61E-05	2.43504
NM_175429 // Kctd12b // potassium channel tetramerisation domain containing 12b // X F3	Kctd12b	2.71E-05	2.43596
NM_001165256 // Dcaf4 // DDB1 and CUL4 associated factor 4 // 12|12 D3 // 73828 /// NM_	Dcaf4	1.88E-05	2.43656
NM_029665 // Ipo11 // importin 11 // 13 D2.1|13 // 76582 /// XR_382746 // Ipo11 // impo	Ipo11	9.01E-05	2.44157
---		0.00196459	2.44286
NM_026283 // Samd8 // sterile alpha motif domain containing 8 // 14|14 B // 67630 /// X	Samd8	0.000121553	2.44395
---		0.000899052	2.44471
NM_138753 // Hexim1 // hexamethylene bis-acetamide inducible 1 // 11 E1|11 // 192231 //	Hexim1	5.33E-06	2.44516

NM_016845 // Acrbp // proacrosin binding protein // 6|6 F2 // 54137 /// NM_001127340 //	Acrbp	9.17E-05	2.44516
---		0.000454592	2.44601
NM_027477 // Zfp398 // zinc finger protein 398 // 6|6 B3 // 272347 /// NM_173034 // Zfp	Zfp398	0.0049031	2.4473
NM_053214 // Myo1f // myosin IF // 17 B-C|17 17.98 cM // 17916 /// ENSMUST00000087605 /	Myo1f	4.92E-06	2.44827
NM_025578 // Mrps25 // mitochondrial ribosomal protein S25 // 6|6 D3 // 64658 /// ENSMU	Mrps25	0.00543108	2.45216
NM_153083 // Thtpa // thiamine triphosphatase // 14 C1|14 // 105663 /// ENSMUST00000050	Thtpa	0.00021016	2.45217
NM_010559 // Il6ra // interleukin 6 receptor, alpha // 3 F1|3 39.19 cM // 16194 /// ENS	Il6ra	2.30E-07	2.45231
NM_001205353 // Gramd4 // GRAM domain containing 4 // 15 E2|15 // 223752 /// NM_172611	Gramd4	0.000145638	2.45262
XM_006514220 // Tmem198b // transmembrane protein 198b // 10 D3|10 // 73827 /// XM_0065	Tmem198b	0.00014918	2.45274
NM_145612 // Zfp810 // zinc finger protein 810 // 9 A3|9 // 235050 /// ENSMUST000000862	Zfp810	0.000335069	2.45301
NM_001146199 // Ptpn21 // protein tyrosine phosphatase, non-receptor type 21 // 12|12 F	Ptpn21	0.000157261	2.4537
NM_029037 // Pomk // protein-O-mannose kinase // 8|8 A3 // 74653 /// ENSMUST00000061850	Pomk	0.000365969	2.45792
NM_001146153 // Homer3 // homer homolog 3 (Drosophila) // 8|8 C1 // 26558 /// NM_011984	Homer3	0.000405092	2.45951
---		5.90E-08	2.45981
NM_001159907 // Gm17296 // predicted gene, 17296 // 8 E2|8 // 212728 /// XM_006530818 /	Gm17296	0.00320063	2.46235
NM_026539 // Chd1l // chromodomain helicase DNA binding protein 1-like // 3|3 F2 // 680	Chd1l	8.72E-06	2.46357
---		0.000550353	2.46388
NM_013630 // Pkd1 // polycystic kidney disease 1 homolog // 17 A3.3|17 12.4 cM // 18763	Pkd1	6.34E-05	2.4646
NM_028065 // Cnpy3 // canopy 3 homolog (zebrafish) // 17|17 C // 72029 /// ENSMUST00000	Cnpy3	1.43E-05	2.46461
NM_019551 // Tdp2 // tyrosyl-DNA phosphodiesterase 2 // 13 A3.1|13 10.7 cM // 56196 ///	Tdp2	0.000896154	2.46637
ENSMUST00000166047 // Gm17122 // predicted gene 17122 // --- // --- /// AK188192 // Cor	Gm17122	3.48E-05	2.46655
NM_010424 // Hfe // hemochromatosis // 13 A2-A4|13 9.88 cM // 15216 /// XM_006516556 //	Hfe	2.48E-05	2.46719
NM_138607 // Fam50a // family with sequence similarity 50, member A // X A7.3|X // 1081	Fam50a	8.73E-06	2.46738
NR_045266 // Gm15545 // predicted gene 15545 // 7|7 29.07 cM // 100502630 /// ENSMUST00	Gm15545	0.00297772	2.47112
NM_172280 // 2210018M11Rik // RIKEN cDNA 2210018M11 gene // 7 E2|7 // 233545 /// XR_378	2210018M11Ri	7.71E-06	2.47311
NM_001113550 // 4833420G17Rik // RIKEN cDNA 4833420G17 gene // 13 D2.3|13 // 67392 ///	4833420G17Ril	2.95E-06	2.4732
NM_007760 // Crat // carnitine acetyltransferase // 2 B|2 21.69 cM // 12908 /// ENSMUST	Crat	3.17E-06	2.47341
NM_183195 // Marveld1 // MARVEL (membrane-associating) domain containing 1 // 19 C3|19	Marveld1	0.000148247	2.47347
NM_007421 // Adssl1 // adenylosuccinate synthetase like 1 // 12 F1|12 // 11565 /// ENSM	Adssl1	5.98E-07	2.47535
NM_023397 // Mdp1 // magnesium-dependent phosphatase 1 // 14 C3|14 // 67881 /// NR_0283	Mdp1	7.14E-05	2.47638
XR_401827 // LOC102643030 // uncharacterized LOC102643030 // --- // 102643030 /// XR_40	LOC102643030	0.00629546	2.47673
NM_011273 // Xpr1 // xenotropic and polytropic retrovirus receptor 1 // 1 G3|1 66.49 cM	Xpr1	1.91E-07	2.47696
NM_025412 // Pycrl // pyrroline-5-carboxylate reductase-like // 15|15 E1 // 66194 /// X	Pycrl	0.00324916	2.47756
NM_026160 // Map1lc3b // microtubule-associated protein 1 light chain 3 beta // 8 E1|8	Map1lc3b	5.65E-05	2.47789
NM_001163847 // Tbc1d24 // TBC1 domain family, member 24 // 17 A3.3|17 // 224617 /// NM	Tbc1d24	0.00250299	2.47828
NM_026674 // Aph1c // anterior pharynx defective 1c homolog (C. elegans) // 9 C|9 // 68	Aph1c	8.54E-06	2.47925
NM_026319 // Ift74 // intraflagellar transport 74 // 4 C5|4 // 67694 /// XM_006503324 /	Ift74	1.08E-06	2.47988
NM_029394 // Snx24 // sorting nexing 24 // 18 D1|18 // 69226 /// XM_006526220 // Snx24	Snx24	1.73E-06	2.4833
NM_001270495 // Tmem254b // transmembrane protein 254b // 14 A3|14 // 100039257 /// NM_	Tmem254b	0.000190748	2.48407
NM_001163640 // Chn2 // chimerin 2 // 6 B3|6 // 69993 /// NM_023543 // Chn2 // chimerin	Chn2	0.000358745	2.48463
NM_010957 // Ogg1 // 8-oxoguanine DNA-glycosylase 1 // 6 E-F1|6 52.75 cM // 18294 /// E	Ogg1	8.35E-06	2.48542
NM_025556 // Coprs // coordinator of PRMT5, differentiation stimulator // 8 A1.1|8 // 6	Coprs	0.000455255	2.48558
NM_001205068 // Jmjd4 // jumonji domain containing 4 // 11 B1.3|11 // 194952 /// NM_178	Jmjd4	0.0010577	2.48663
NM_001252573 // Slc35c2 // solute carrier family 35, member C2 // 2 H3|2 85.53 cM // 22	Slc35c2	0.000370199	2.49205
NM_133706 // Tmem97 // transmembrane protein 97 // 11 B5|11 46.74 cM // 69071 /// ENSMU	Tmem97	0.000225917	2.49221
NM_198033 // Setx // senataxin // 2 A3|2 // 269254 /// ENSMUST00000061578 // Setx // se	Setx	4.68E-06	2.49244
NM_199301 // Mtg1 // mitochondrial GTPase 1 homolog (S. cerevisiae) // 7 F4|7 // 212508	Mtg1	0.00145106	2.49625
NM_172903 // Man2a2 // mannosidase 2, alpha 2 // 7 D2|7 // 140481 /// ENSMUST0000009834	Man2a2	7.81E-08	2.49761
---		0.00627641	2.50042
NM_178364 // Zfp369 // zinc finger protein 369 // 13 B3|13 // 170936 /// ENSMUST0000012	Zfp369	0.000128323	2.50182
NM_145425 // Wdpcp // WD repeat containing planar cell polarity effector // 11 A3.1|11	Wdpcp	0.00272914	2.5032
NM_001161111 // Pqlc3 // PQ loop repeat containing // 12 A1.1|12 // 217430 /// NM_17257	Pqlc3	4.58E-08	2.50356
NM_001162416 // Pfkfb2 // 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 // 1 E4	Pfkfb2	3.51E-05	2.5051
---		0.000725877	2.50568
NM_133738 // Antxr2 // anthrax toxin receptor 2 // 5 E3|5 // 71914 /// ENSMUST000000312	Antxr2	3.66E-06	2.50676
ENSMUST00000169406 // Gm1818 // predicted gene 1818 // 12 B3|12 // 217536 /// M74555 //	Gm1818	0.000285459	2.50919
NM_024229 // Pcyt2 // phosphate cytidylyltransferase 2, ethanolamine // 11 E2|11 // 686	Pcyt2	5.55E-05	2.51029
NM_013881 // Ulk2 // unc-51 like kinase 2 // 11 B2|11 // 29869 /// XM_006533508 // Ulk2	Ulk2	1.10E-05	2.51468
NM_008279 // Map4k1 // mitogen-activated protein kinase kinase kinase kinase 1 // 7 B1|	Map4k1	1.22E-06	2.51493
NM_008494 // Lfng // LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase // 5	Lfng	4.29E-06	2.51572
NM_001270495 // Tmem254b // transmembrane protein 254b // 14 A3|14 // 100039257 /// NM_	Tmem254b	0.00052874	2.51587
NM_001033142 // Rnf166 // ring finger protein 166 // 8 E1|8 // 68718 /// XM_006531336 /	Rnf166	3.30E-05	2.5164
NM_010813 // Mnt // max binding protein // 11 B-C|11 45.76 cM // 17428 /// XM_006532403	Mnt	0.000186951	2.51664
NR_033628 // AA474331 // expressed sequence AA474331 // 10 B1|10 // 213332 /// ENSMUST0	AA474331	0.000709409	2.51671
NM_001127330 // Pparg // peroxisome proliferator activated receptor gamma // 6 E3-F1|6	Pparg	4.02E-07	2.51843
NM_001033872 // Smagp // small cell adhesion glycoprotein // 15 F1|15 // 207818 /// NM_	Smagp	0.000317397	2.51906
NM_178620 // Mfsd11 // major facilitator superfamily domain containing 11 // 11 E2|11 /	Mfsd11	1.09E-06	2.52018
NM_145456 // Zswim6 // zinc finger SWIM-type containing 6 // 13 D2.1|13 // 67263 /// EN	Zswim6	1.34E-05	2.5226
NM_001081152 // Npat // nuclear protein in the AT region // 9 A5.3|9 29.12 cM // 244879	Npat	7.36E-06	2.52364
---		0.00313702	2.52399
NM_001199060 // Wdr12 // WD repeat domain 12 // 1|1 C1-C2 // 57750 /// NM_001199061 //	Wdr12	5.76E-06	2.52426
NM_031156 // Ide // insulin degrading enzyme // 19 C2|19 32.24 cM // 15925 /// ENSMUST0	Ide	5.67E-07	2.52451
NM_001038700 // Fnbp1 // formin binding protein 1 // 2 B|2 // 14269 /// NM_001177648 //	Fnbp1	2.53E-05	2.52463
NM_024264 // Cyp27a1 // cytochrome P450, family 27, subfamily a, polypeptide 1 // 1 C3|	Cyp27a1	2.17E-05	2.52561
AK132205 // Gm10554 // predicted gene 10554 // 18 A1|18 // 100038541	Gm10554	0.00277382	2.52606
---		0.00358885	2.52767
NM_080289 // Grhpr // glyoxylate reductase/hydroxypyruvate reductase // 4|4 B2 // 76238	Grhpr	0.00141216	2.52854
NM_153391 // Wdr19 // WD repeat domain 19 // 5 C3.1|5 // 213081 /// ENSMUST00000041892	Wdr19	0.000621094	2.52955
---		0.000182326	2.53016
NM_018797 // Plxnc1 // plexin C1 // 10|10 C3 // 54712 /// XM_006513895 // Plxnc1 // ple	Plxnc1	1.24E-06	2.53259
NM_010111 // Efnb2 // ephrin B2 // 8 A1.1|8 3.42 cM // 13642 /// ENSMUST00000001319 //	Efnb2	0.000977263	2.53291
NM_001253808 // Racgap1 // Rac GTPase-activating protein 1 // 15 F1|15 // 26934 /// NM_	Racgap1	8.39E-06	2.53525
NM_001082532 // Pigyl // phosphatidylinositol glycan anchor biosynthesis, class Y-like	Pigyl	0.00143023	2.5359
NM_001134717 // 2810006K23Rik // RIKEN cDNA 2810006K23 gene // 5 F|5 // 72650 /// NM_02	2810006K23Rik	0.00435388	2.53622
NM_001113470 // Ctdsp2 // CTD (carboxy-terminal domain, RNA polymerase II, polypeptide	Ctdsp2	6.81E-06	2.53664
NM_177586 // Eif5a2 // eukaryotic translation initiation factor 5A2 // 3 A3|3 // 208691	Eif5a2	2.20E-06	2.53727
NM_177878 // Mblac1 // metallo-beta-lactamase domain containing 1 // 5 G2|5 // 330216 /	Mblac1	0.00650173	2.53746
ENSMUST00000028807 // Ivd // isovaleryl coenzyme A dehydrogenase // 2 E4-E5|2 // 56357	Ivd	2.72E-06	2.53899
NM_008043 // Frat1 // frequently rearranged in advanced T cell lymphomas // 19 C3|19 35	Frat1	0.00159872	2.54058

NM_028994 // Pck2 // phosphoenolpyruvate carboxykinase 2 (mitochondrial) // 14 C1|14 28	Pck2	0.00104994	2.54201
NM_001081344 // Stxbp5 // syntaxin binding protein 5 (tomosyn) // 10|10 A2 // 78808 ///	Stxbp5	1.40E-06	2.54504
XM_006513283 // Lss // lanosterol synthase // 10 C1|10 39.1 cM // 16987 /// NM_146006 /	Lss	7.77E-05	2.5457
BC099943 // Mettl4 // methyltransferase like 4 // 17 E5|17 // 76781 /// NM_176917 // Me	Mettl4	3.97E-07	2.54633
NM_010295 // Gclc // glutamate-cysteine ligase, catalytic subunit // 9 D-E|9 43.36 cM /	Gclc	3.40E-08	2.54667
---		0.000483835	2.54787
NM_001198570 // Abi2 // abl-interactor 2 // 1 C2|1 // 329165 /// NM_001198571 // Abi2 /	Abi2	0.000160514	2.55333
NM_026174 // Entpd4 // ectonucleoside triphosphate diphosphohydrolase 4 // 14 D2|14 //	Entpd4	3.36E-08	2.55511
---		0.00656091	2.55562
ENSMUST00000181570 // Gpr137b-ps // G protein-coupled receptor 137B, pseudogene // 13 A	Gpr137b-ps	0.00307687	2.55676
NM_026633 // Fam195a // family with sequence similarity 195, member A // 17|17 B1 // 68	Fam195a	3.52E-05	2.55911
NM_146001 // Hip1 // huntingtin interacting protein 1 // 5 F-G2|5 75.18 cM // 215114 //	Hip1	1.02E-05	2.55977
NM_184088 // Dennd4c // DENN/MADD domain containing 4C // 4 C4|4 // 329877 /// ENSMUST0	Dennd4c	3.20E-06	2.56546
NM_001291211 // Pcmtd2 // protein-L-isoaspartate (D-aspartate) O-methyltransferase doma	Pcmtd2	8.42E-06	2.56756
NM_013692 // Klf10 // Kruppel-like factor 10 // 15 B3.1|15 // 21847 /// XM_006520046 //	Klf10	5.89E-06	2.56863
ENSMUST00000049948 // Asrgl1 // asparaginase like 1 // 19 A|19 // 66514 /// NM_025610 /	Asrgl1	0.000376675	2.57046
NM_001270495 // Tmem254b // transmembrane protein 254b // 14 A3|14 // 100039257 /// NM_	Tmem254b	0.000636171	2.57105
NM_027495 // Tmem144 // transmembrane protein 144 // 3|3 F1 // 70652 /// XM_006502057 /	Tmem144	0.000249669	2.57201
ENSMUST00000172910 // Gm9581 // predicted gene 9581 // --- // ---	Gm9581	0.00171962	2.57205
NM_026028 // Ccdc77 // coiled-coil domain containing 77 // 6 F1|6 // 67200 /// XM_00650	Ccdc77	0.00158288	2.57539
NM_001081264 // Alg6 // asparagine-linked glycosylation 6 (alpha-1,3,-glucosyltransfera	Alg6	1.06E-05	2.57557
ENSMUST00000102484 // Ddi2 // DNA-damage inducible protein 2 // 4 E1|4 // 68817 /// NM_	Ddi2	5.56E-08	2.57811
NM_153591 // Nars2 // asparaginyl-tRNA synthetase 2 (mitochondrial)(putative) // 7 E1|7	Nars2	3.57E-06	2.57902
NM_183116 // Slc18b1 // solute carrier family 18, subfamily B, member 1 // 10 A3-A4|10	Slc18b1	0.00199792	2.57917
NM_178213 // Hist2h2ab // histone cluster 2, H2ab // 3 F1-F2|3 // 621893 /// ENSMUST000	Hist2h2ab	0.00468279	2.57951
NM_001080949 // Ttc5 // tetratricopeptide repeat domain 5 // 14 C1|14 // 219022 /// NM_	Ttc5	9.76E-05	2.58052
NM_133198 // Pygl // liver glycogen phosphorylase // 12 C2|12 29.01 cM // 110095 /// EN	Pygl	2.47E-05	2.58065
NM_026740 // Slc46a1 // solute carrier family 46, member 1 // 11 B5|11 46.74 cM // 5246	Slc46a1	0.00032836	2.58084
NM_019537 // Psmg1 // proteasome (prosome, macropain) assembly chaperone 1 // 16 C4|16	Psmg1	0.00103021	2.58326
NM_009567 // Zfp93 // zinc finger protein 93 // 7 A3|7 10.27 cM // 22755	Zfp93	0.00286977	2.58334
NR_027993 // Gm3414 // predicted gene 3414 // 5 B3|5 // 100041576 /// XM_006503821 // L	Gm3414	0.00110503	2.58655
NM_001177878 // Phka2 // phosphorylase kinase alpha 2 // X F3-F4|X 73.95 cM // 110094 /	Phka2	2.63E-07	2.58842
---		0.000463053	2.59137
---		0.00130251	2.59279
NM_172578 // Mis18bp1 // MIS18 binding protein 1 // 12 C1|12 // 217653 /// ENSMUST00000	Mis18bp1	8.84E-07	2.59283
NM_001037937 // Deptor // DEP domain containing MTOR-interacting protein // 15 D1|15 21	Deptor	0.000459827	2.59294
NM_172600 // Tmem260 // transmembrane protein 260 // 14 C1|14 // 218989 /// XM_00651883	Tmem260	3.33E-05	2.59761
NM_134126 // Ift140 // intraflagellar transport 140 // 17 A3.3|17 // 106633 /// XM_0065	Ift140	4.33E-05	2.60054
NM_178724 // Harbi1 // harbinger transposase derived 1 // 2 E1|2 // 241547 /// ENSMUST0	Harbi1	0.00026665	2.60199
NM_008832 // Phka1 // phosphorylase kinase alpha 1 // X D|X 45.47 cM // 18679 /// NM_17	Phka1	0.000675168	2.6032
NM_010146 // Epm2a // epilepsy, progressive myoclonic epilepsy, type 2 gene alpha // 10	Epm2a	0.000209107	2.60438
NM_028064 // Slc39a4 // solute carrier family 39 (zinc transporter), member 4 // 15 D3|	Slc39a4	9.75E-05	2.60571
NM_001168386 // Ccdc125 // coiled-coil domain containing 125 // 13 D1|13 // 76041 /// N	Ccdc125	6.83E-06	2.60586
NM_145599 // Tmem184c // transmembrane protein 184C // 8 C1|8 // 234463 /// XM_00653085	Tmem184c	6.48E-07	2.60714
NM_001033337 // Ttc38 // tetratricopeptide repeat domain 38 // 15 E2|15 // 239570 /// X	Ttc38	1.84E-05	2.60878
NM_001284402 // P2rx7 // purinergic receptor P2X, ligand-gated ion channel, 7 // 5 F|5	P2rx7	4.97E-07	2.61205
NM_017476 // Akap8l // A kinase (PRKA) anchor protein 8-like // 17|17 B2 // 54194 /// X	Akap8l	0.00103285	2.61208
NM_178772 // Nceh1 // neutral cholesterol ester hydrolase 1 // 3 A3|3 // 320024 /// ENS	Nceh1	2.10E-07	2.61276
NM_007620 // Cbr1 // carbonyl reductase 1 // 16 C4|16 54.53 cM // 12408 /// XM_00654334	Cbr1	0.000100905	2.61444
NM_001001333 // Hexdc // hexosaminidase (glycosyl hydrolase family 20, catalytic domain	Hexdc	0.000227731	2.61523
NM_133740 // Prmt3 // protein arginine N-methyltransferase 3 // 7 B5|7 // 71974 /// ENS	Prmt3	6.03E-07	2.61634
ENSMUST00000123693 // Ptgr2 // prostaglandin reductase 2 // 12|12 D3 // 77219 /// ENSMU	Ptgr2	6.57E-06	2.61745
NM_001081411 // Sclt1 // sodium channel and clathrin linker 1 // 3|3 C // 67161 /// ENS	Sclt1	0.000278995	2.61937
NM_146033 // Ankmy2 // ankyrin repeat and MYND domain containing 2 // 12 A3|12 // 21747	Ankmy2	2.03E-06	2.62021
NM_146251 // Pnpla7 // patatin-like phospholipase domain containing 7 // 2 A3|2 // 2412	Pnpla7	5.01E-06	2.6207
NM_001081323 // Mphosph9 // M-phase phosphoprotein 9 // 5 F|5 // 269702 /// NM_00127786	Mphosph9	2.09E-05	2.62149
NM_001033219 // Slc45a4 // solute carrier family 45, member 4 // 15 D3|15 // 106068 ///	Slc45a4	0.000189591	2.62398
NM_001159365 // Cep97 // centrosomal protein 97 // 16 C1.1|16 // 74201 /// NM_001159366	Cep97	0.000293145	2.62479
NM_001033258 // D10Bwg1379e // DNA segment, Chr 10, Brigham & Womens Genetics 1379 expr	D10Bwg1379e	1.42E-05	2.63542
NM_025823 // Pcyox1 // prenylcysteine oxidase 1 // 6 D1|6 // 66881 /// ENSMUST000000320	Pcyox1	5.44E-08	2.64256
---		0.00157426	2.64464
NM_001081112 // Ankrd26 // ankyrin repeat domain 26 // 6 F1|6 // 232339 /// ENSMUST0000	Ankrd26	0.000620317	2.64518
NM_001285463 // Carf // calcium response factor // 1 C2|1 // 241066 /// NM_001285473 //	Carf	0.00020665	2.64554
NR_045187 // 4833417C18Rik // RIKEN cDNA 4833417C18 gene // 11|11 // 73906 /// ENSMUST0	4833417C18Rik	0.000572211	2.6476
AK047378 // Chst10 // carbohydrate sulfotransferase 10 // 1 B|1 // 98388 /// NM_145142	Chst10	0.000236003	2.64871
NM_009908 // Cmas // cytidine monophospho-N-acetylneuraminic acid synthetase // 6 G3|6	Cmas	4.01E-07	2.65031
NM_001145967 // Atg4c // autophagy related 4C, cysteine peptidase // 4 C6|4 // 242557 /	Atg4c	8.23E-06	2.65214
NM_146184 // B3gnt8 // UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8 //	B3gnt8	0.000728594	2.65464
NM_146171 // Ncapd2 // non-SMC condensin I complex, subunit D2 // 6|6 F2 // 68298 /// E	Ncapd2	0.000460065	2.65481
NM_008611 // Mmp8 // matrix metallopeptidase 8 // 9 A1|9 // 17394 /// ENSMUST0000001876	Mmp8	8.32E-05	2.65492
NM_175507 // Slc35g1 // solute carrier family 35, member G1 // 19 C3|19 // 240660 /// E	Slc35g1	4.22E-05	2.66085
NM_008397 // Itga6 // integrin alpha 6 // 2 C2-C3|2 42.79 cM // 16403 /// NM_001277970	Itga6	6.81E-06	2.66139
NM_145382 // Fam193b // family with sequence similarity 193, member B // 13 B1|13 // 21	Fam193b	0.00344414	2.66763
NM_001281980 // Lrmp // lymphoid-restricted membrane protein // 6 G3|6 77.34 cM // 1697	Lrmp	1.57E-05	2.66884
NM_009370 // Tgfbr1 // transforming growth factor, beta receptor I // 4 B1|4 26.02 cM /	Tgfbr1	1.43E-06	2.66997
---		0.00579942	2.67091
NM_001276452 // Slc17a5 // solute carrier family 17 (anion/sugar transporter), member 5	Slc17a5	2.27E-06	2.67579
NM_007533 // Bckdha // branched chain ketoacid dehydrogenase E1, alpha polypeptide // 7	Bckdha	4.25E-05	2.67718
NM_138586 // Exosc5 // exosome component 5 // 7 A3|7 13.96 cM // 27998 /// NR_104358 //	Exosc5	0.000516586	2.67782
NM_029420 // Slx1b // SLX1 structure-specific endonuclease subunit homolog B (S. cerevi	Slx1b	0.000402117	2.67802
NM_183034 // Plekhm1 // pleckstrin homology domain containing, family M (with RUN domai	Plekhm1	8.10E-06	2.67871
---		0.000569009	2.68117
NM_172562 // Tada2a // transcriptional adaptor 2A // 11 C|11 // 217031 /// XM_006532989	Tada2a	5.22E-06	2.68375
NM_001081040 // Coq10a // coenzyme Q10 homolog A (yeast) // 10 D3|10 // 210582 /// XM_0	Coq10a	4.72E-05	2.68466
NM_001253692 // Elmod3 // ELMO/CED-12 domain containing 3 // 6 C1|6 // 232089 /// NM_14	Elmod3	0.00209912	2.68583
NM_146069 // Nrros // negative regulator of reactive oxygen species // 16 B2|16 // 2241	Nrros	4.77E-07	2.69018
NM_001025250 // Vegfa // vascular endothelial growth factor A // 17 C|17 22.79 cM // 22	Vegfa	6.80E-09	2.69066
---		0.00022364	2.69373
NR_036450 // Gm14403 // predicted gene 14403 // 2 H4|2 // 433520	Gm14403	0.000620805	2.69477

NM_001290782 // Accs // 1-aminocyclopropane-1-carboxylate synthase (non-functional) //	Accs	5.27E-05	2.69505
NM_001033441 // Alg10b // asparagine-linked glycosylation 10B (alpha-1,2-glucosyltransf	Alg10b	1.68E-06	2.69672
NM_001252220 // Nbr1 // neighbor of Brca1 gene 1 // 11 D|11 65.36 cM // 17966 /// NM_00	Nbr1	2.75E-07	2.69945
NM_007496 // Zfhx3 // zinc finger homeobox 3 // 8|8 E1 // 11906 /// XM_006530586 // Zfh	Zfhx3	2.65E-05	2.69953
XR_401386 // 4930555A03Rik // RIKEN cDNA 4930555A03 gene // 3|3 // 100504653 /// AK0088	4930555A03Rik	0.00203385	2.70075
NM_133976 // Imp3 // IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) // 9 B	Imp3	4.06E-05	2.7063
NM_001177568 // Gm14420 // predicted gene 14420 // 2 H4|2 // 628308	Gm14420	1.60E-05	2.7064
---		0.00449835	2.70678
NM_001199304 // Atxn1 // ataxin 1 // 13 A5|13 21.98 cM // 20238 /// NM_001199305 // Atx	Atxn1	0.000151581	2.70836
NM_011305 // Rxra // retinoid X receptor alpha // 2 A3|2 19.38 cM // 20181 /// ENSMUST0	Rxra	3.99E-06	2.70996
NM_001017983 // Foxred2 // FAD-dependent oxidoreductase domain containing 2 // 15 E1|15	Foxred2	0.000137655	2.71018
---		0.00377473	2.71051
---		0.00425176	2.71079
NM_028959 // Cep72 // centrosomal protein 72 // 13 C1|13 // 74470 /// ENSMUST0000003645	Cep72	0.000147891	2.71452
NM_001039472 // Kif21b // kinesin family member 21B // 1 E4|1 59.61 cM // 16565 /// ENS	Kif21b	5.78E-05	2.71461
---		3.04E-05	2.71528
ENSMUST00000140646 // Gm15513 // predicted gene 15513 // --- // ---	Gm15513	0.00195072	2.71662
NM_001081278 // Tbc1d4 // TBC1 domain family, member 4 // 14 E2.3|14 // 210789 /// XM_0	Tbc1d4	2.58E-05	2.71812
NM_025790 // Acot13 // acyl-CoA thioesterase 13 // 13|13 A3.2 // 66834 /// ENSMUST00000	Acot13	3.87E-06	2.72298
NM_011828 // Hs2st1 // heparan sulfate 2-O-sulfotransferase 1 // 3 H2|3 // 23908 /// XM	Hs2st1	4.53E-05	2.72371
NM_010560 // Il6st // interleukin 6 signal transducer // 13 D2.2|13 63.73 cM // 16195 /	Il6st	5.93E-08	2.72464
NM_172146 // Ppat // phosphoribosyl pyrophosphate amidotransferase // 5 C3.3|5 // 23132	Ppat	0.00024324	2.72522
NM_139138 // Emr4 // EGF-like module containing, mucin-like, hormone receptor-like sequ	Emr4	0.00070726	2.72687
NM_145223 // Alms1 // Alstrom syndrome 1 // 6 C3|6 // 236266 /// ENSMUST00000072018 //	Alms1	0.00098987	2.72746
NM_001164426 // Kcnk13 // potassium channel, subfamily K, member 13 // 12 E|12 // 21782	Kcnk13	0.000722092	2.72906
NM_001130416 // Hdac6 // histone deacetylase 6 // X A1.1|X 3.58 cM // 15185 /// NM_0104	Hdac6	3.11E-05	2.72992
NM_001115018 // Suv420h2 // suppressor of variegation 4-20 homolog 2 (Drosophila) // 7	Suv420h2	9.28E-05	2.73123
NM_010247 // Xrcc6 // X-ray repair complementing defective repair in Chinese hamster ce	Xrcc6	3.25E-05	2.73189
NM_028131 // Cenpn // centromere protein N // 8 E1|8 // 72155 /// ENSMUST00000034205 //	Cenpn	0.000153619	2.73318
NM_172631 // Ldlrad4 // low density lipoprotein receptor class A domain containing 4 //	Ldlrad4	1.63E-05	2.73513
NM_153587 // Rps6ka5 // ribosomal protein S6 kinase, polypeptide 5 // 12 E|12 // 73086	Rps6ka5	8.52E-05	2.73631
---		0.000657977	2.73909
NM_177366 // Gpr157 // G protein-coupled receptor 157 // 4 E2|4 // 269604 /// ENSMUST00	Gpr157	5.49E-05	2.73919
NM_023203 // Dctpp1 // dCTP pyrophosphatase 1 // 7 F3|7 // 66422 /// ENSMUST00000035276	Dctpp1	0.0003108	2.74319
NM_027100 // Rwdd2a // RWD domain containing 2A // 9 E3.1|9 // 69519 /// ENSMUST0000003	Rwdd2a	0.00402283	2.74995
NM_001271357 // Flcn // folliculin // 11 B1.3|11 // 216805 /// NR_073164 // Flcn // fol	Flcn	8.14E-08	2.75593
NM_177151 // Vps13b // vacuolar protein sorting 13B (yeast) // 15 B3.1|15 // 666173 ///	Vps13b	5.11E-08	2.75676
NM_001159572 // 4632428N05Rik // RIKEN cDNA 4632428N05 gene // 10 B4|10 // 74048 /// NM	4632428N05Rik	3.16E-07	2.75901
NM_001195537 // Smpd5 // sphingomyelin phosphodiesterase 5 // 15 D3|15 // 100503915 ///	Smpd5	0.000344613	2.76489
NM_025864 // Tmem206 // transmembrane protein 206 // 1 H6|1 // 66950 /// ENSMUST0000002	Tmem206	6.16E-06	2.76633
NM_145359 // Ubald1 // UBA-like domain containing 1 // 16 A1|16 // 207740 /// ENSMUST00	Ubald1	7.92E-05	2.7665
NM_001033606 // Acsl3 // acyl-CoA synthetase long-chain family member 3 // 1 C4|1 40.84	Acsl3	0.000146507	2.76697
NM_175265 // Bora // bora, aurora kinase A activator // 14 E2.2|14 // 77744 /// XM_0065	Bora	0.00263326	2.77277
NM_001285917 // Dapk1 // death associated protein kinase 1 // 13 B2|13 32.53 cM // 6963	Dapk1	1.91E-07	2.77487
NM_001008501 // Zfp760 // zinc finger protein 760 // 17 A3.2-A3.3|17 // 240034 /// ENSM	Zfp760	0.00035331	2.77606
NM_001163734 // Rrp1b // ribosomal RNA processing 1 homolog B (S. cerevisiae) // 17 B1|	Rrp1b	1.01E-05	2.77677
NM_175383 // B3gnt1 // UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1 //	B3gnt1	7.39E-06	2.77801
XR_393428 // Gm11423 // predicted gene 11423 // 11|11 50.23 cM // 100503272 /// ENSMUST	Gm11423	8.14E-07	2.78144
NM_009012 // Rad50 // RAD50 homolog (S. cerevisiae) // 11 A5-B1|11 31.98 cM // 19360 //	Rad50	1.93E-06	2.78989
NM_001290792 // Wdr45 // WD repeat domain 45 // X A1.1|X 3.48 cM // 54636 /// NM_001290	Wdr45	1.16E-07	2.79302
NM_029762 // Hyls1 // hydrolethalus syndrome 1 // 9 A4|9 // 76832 /// ENSMUST0000011511	Hyls1	0.000414415	2.79327
NM_001166406 // Kif20a // kinesin family member 20A // 18 B1|18 18.69 cM // 19348 /// N	Kif20a	8.35E-06	2.79463
NM_001014981 // Wdr7 // WD repeat domain 7 // 18|18 D1-E3 // 104082 /// ENSMUST00000072	Wdr7	9.79E-06	2.7956
NM_009266 // Sephs2 // selenophosphate synthetase 2 // 7 F3|7 69.43 cM // 20768 /// AK0	Sephs2	6.19E-06	2.79939
AK032971 // Gm11974 // predicted gene 11974 // 11 A1|11 // 100041286	Gm11974	0.0057794	2.80212
ENSMUST00000082675 // Gm25635 // predicted gene, 25635 // --- // ---	Gm25635	0.000228135	2.80446
---		0.00411694	2.80481
NM_145564 // Fbxo21 // F-box protein 21 // 5 F|5 // 231670 /// ENSMUST00000035579 // Fb	Fbxo21	1.47E-05	2.80492
---		2.35E-05	2.80698
NM_001081415 // Samd1 // sterile alpha motif domain containing 1 // 8 C3|8 // 666704 //	Samd1	1.55E-05	2.81058
NM_011638 // Tfrc // transferrin receptor // 16 B3|16 23.06 cM // 22042 /// ENSMUST0000	Tfrc	4.61E-08	2.81278
NM_029600 // Abcc3 // ATP-binding cassette, sub-family C (CFTR/MRP), member 3 // 11 D|1	Abcc3	2.73E-08	2.81726
ENSMUST00000001331 // Myg1 // melanocyte proliferating gene 1 // 15 F3|15 // 60315 ///	Myg1	1.20E-05	2.81867
NM_001122818 // Pnpla6 // patatin-like phospholipase domain containing 6 // 8 A1.1|8 1.	Pnpla6	1.61E-05	2.81947
NM_001042655 // Tbc1d17 // TBC1 domain family, member 17 // 7 B4|7 // 233204 /// ENSMUS	Tbc1d17	3.21E-05	2.82064
ENSMUST00000085206 // Slc25a36 // solute carrier family 25, member 36 // 9 E3.3|9 // 19	Slc25a36	1.11E-06	2.82263
NM_001256522 // C330006A16Rik // RIKEN cDNA C330006A16 gene // 2 A3|2 // 109299	C330006A16Rik	0.00242339	2.82506
NM_133976 // Imp3 // IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) // 9 B	Imp3	0.000218844	2.82547
XM_006518799 // Tsc22d1 // TSC22 domain family, member 1 // 14 D3|14 40.44 cM // 21807	Tsc22d1	4.40E-05	2.82556
NM_001039534 // Pstk // phosphoseryl-tRNA kinase // 7 F3|7 // 214580 /// ENSMUST0000007	Pstk	1.06E-05	2.82783
NM_173733 // Suox // sulfite oxidase // 10 D3|10 // 211389 /// ENSMUST00000054764 // Su	Suox	0.000528703	2.83086
NM_007420 // Adrb2 // adrenergic receptor, beta 2 // 18 E1|18 35.1 cM // 11555 /// ENSM	Adrb2	0.000699832	2.83144
NM_173865 // Slc41a1 // solute carrier family 41, member 1 // 1 E4|1 // 98396 /// ENSMU	Slc41a1	2.56E-06	2.83278
NM_025370 // Aaed1 // AhpC/TSA antioxidant enzyme domain containing 1 // 13 B3|13 // 66	Aaed1	4.75E-07	2.83451
NM_001040130 // Tmem141 // transmembrane protein 141 // 2 A3|2 17.57 cM // 51875 /// NM	Tmem141	1.90E-05	2.84082
NM_028390 // Anln // anillin, actin binding protein // 9|9 A4 // 68743 /// XM_006510581	Anln	0.000458143	2.841
NM_175542 // Rttn // rotatin // 18 E4|18 // 246102 /// ENSMUST00000023828 // Rttn // ro	Rttn	1.37E-05	2.84105
NM_026641 // Ift80 // intraflagellar transport 80 // 3|3 E2 // 68259 /// XM_006501966 /	Ift80	0.000161471	2.84195
NM_194348 // Atg2a // autophagy related 2A // 19 A|19 // 329015 /// ENSMUST00000045351	Atg2a	1.42E-05	2.84237
NM_027279 // Mettl18 // methyltransferase like 18 // 1 H2.2|1 // 69962 /// ENSMUST00000	Mettl18	0.000133066	2.8458
NM_022017 // Trpv4 // transient receptor potential cation channel, subfamily V, member	Trpv4	0.000279161	2.85691
NM_175403 // Mlec // malectin // 5 F|5 55.99 cM // 109154 /// ENSMUST00000053271 // Mle	Mlec	1.81E-08	2.85731
NM_001168615 // Tifab // TRAF-interacting protein with forkhead-associated domain, fami	Tifab	1.04E-06	2.85788
NM_001168288 // Arhgap39 // Rho GTPase activating protein 39 // 15 D3|15 36.28 cM // 22	Arhgap39	0.000120001	2.85837
NM_053169 // Trim16 // tripartite motif-containing 16 // 11 B2|11 // 94092 /// ENSMUST0	Trim16	1.59E-05	2.8621
NM_001252654 // Kcnab2 // potassium voltage-gated channel, shaker-related subfamily, be	Kcnab2	0.000212713	2.86355
NM_152801 // Arhgef6 // Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 // X A5|X	Arhgef6	1.39E-05	2.86725
NM_001037937 // Deptor // DEP domain containing MTOR-interacting protein // 15 D1|15 21	Deptor	6.17E-05	2.86776
NM_001110193 // Inpp5d // inositol polyphosphate-5-phosphatase D // 1 C5|1 44.44 cM //	Inpp5d	2.48E-06	2.86954

NR_037996 // Hmga2-ps1 // high mobility group AT-hook 2, pseudogene 1 // 1|1 // 15365	Hmga2-ps1	3.88E-05	2.87222
NM_001177806 // Eif2ak4 // eukaryotic translation initiation factor 2 alpha kinase 4 //	Eif2ak4	1.44E-05	2.87759
NM_030719 // Gatsl2 // GATS protein-like 2 // 5|5 G1 // 80909 /// ENSMUST00000016088 //	Gatsl2	1.74E-05	2.87916
NM_001080557 // Vamp1 // vesicle-associated membrane protein 1 // 6 F3|6 59.32 cM // 22	Vamp1	0.000483196	2.88027
---		1.19E-05	2.88265
NM_177305 // Arl4c // ADP-ribosylation factor-like 4C // 1 D|1 // 320982 /// ENSMUST000	Arl4c	1.70E-06	2.88496
NM_207301 // Wrb // tryptophan rich basic protein // 16 C4|16 // 71446 /// XM_006523091	Wrb	3.66E-05	2.88888
NM_012048 // Polk // polymerase (DNA directed), kappa // 13 D1|13 // 27015 /// XM_00651	Polk	1.22E-05	2.89087
ENSMUST00000001455 // Mef2d // myocyte enhancer factor 2D // 3 F1|3 38.78 cM // 17261 /	Mef2d	5.30E-05	2.89241
NM_181325 // Slc25a15 // solute carrier family 25 (mitochondrial carrier ornithine tran	Slc25a15	1.40E-05	2.89703
NM_130450 // Elovl6 // ELOVL family member 6, elongation of long chain fatty acids (yea	Elovl6	4.22E-05	2.90345
NM_178415 // Bbs9 // Bardet-Biedl syndrome 9 (human) // 9 A3|9 // 319845 /// NM_181316	Bbs9	1.36E-05	2.9039
NM_027188 // Smyd3 // SET and MYND domain containing 3 // 1 H3|1 83.48 cM // 69726 ///	Smyd3	4.24E-06	2.90448
NM_001170537 // Mef2c // myocyte enhancer factor 2C // 13 C3|13 43.68 cM // 17260 /// N	Mef2c	1.06E-07	2.90588
NM_175518 // Tmem245 // transmembrane protein 245 // 4 B3|4 // 242474 /// ENSMUST000000	Tmem245	6.32E-06	2.9085
NM_001037136 // Agap1 // ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 // 1	Agap1	6.71E-06	2.91039
NM_001039551 // Cnnm3 // cyclin M3 // 1 B|1 15.3 cM // 94218 /// NM_053186 // Cnnm3 //	Cnnm3	4.52E-06	2.91081
NM_008212 // Hadh // hydroxyacyl-Coenzyme A dehydrogenase // 3 G3|3 // 15107 /// ENSMUS	Hadh	4.53E-06	2.9119
NM_029128 // Qtrtd1 // queuine tRNA-ribosyltransferase domain containing 1 // 16 B4|16	Qtrtd1	0.000109424	2.91803
NM_013753 // Pald1 // phosphatase domain containing, paladin 1 // 10 B4|10 // 27355 ///	Pald1	0.000307498	2.92377
NM_001205181 // Abhd4 // abhydrolase domain containing 4 // 14 C2|14 // 105501 /// NM_1	Abhd4	1.96E-06	2.92427
NM_199467 // Mms22l // MMS22-like, DNA repair protein // 4 A3|4 // 212377 /// ENSMUST00	Mms22l	6.65E-05	2.92756
NM_010615 // Kif11 // kinesin family member 11 // 19 C2|19 // 16551 /// ENSMUST00000012	Kif11	1.17E-07	2.92922
ENSMUST00000181502 // Gm17586 // predicted gene, 17586 // --- // --- /// AK142663 // Gm	Gm17586	0.000511537	2.93016
ENSMUST00000032803 // Zfp30 // zinc finger protein 30 // 7 B1|7 17.26 cM // 22693 /// E	Zfp30	0.00263603	2.93356
NM_001291910 // Adcy9 // adenylate cyclase 9 // 16 B1|16 2.42 cM // 11515 /// NM_009624	Adcy9	0.000202221	2.9363
NM_001159626 // Hagh // hydroxyacyl glutathione hydrolase // 17 A3.3|17 12.53 cM // 146	Hagh	3.51E-06	2.93872
NM_001290514 // Mospd1 // motile sperm domain containing 1 // X|X A4 // 70380 /// NM_02	Mospd1	4.65E-08	2.94017
NM_008389 // Ipp // IAP promoted placental gene // 4 D1|4 53.2 cM // 16351 /// XM_00650	Ipp	0.000475389	2.94082
ENSMUST00000092720 // 5430403G16Rik // RIKEN cDNA 5430403G16 gene // --- // ---	5430403G16Rik	0.000774639	2.94321
NM_001136236 // Fcrl1 // Fc receptor-like 1 // 3 F1|3 // 229499 /// NM_153090 // Fcrl1	Fcrl1	8.43E-05	2.94322
NM_199029 // Zfp395 // zinc finger protein 395 // 14 D1|14 // 380912 /// ENSMUST0000006	Zfp395	0.000411841	2.94763
NM_001271599 // Sort1 // sortilin 1 // 3 F3|3 // 20661 /// NM_019972 // Sort1 // sortil	Sort1	1.52E-08	2.94881
NM_028773 // Sash3 // SAM and SH3 domain containing 3 // X A4|X // 74131 /// ENSMUST000	Sash3	6.34E-06	2.94917
NM_172619 // Adamts10 // a disintegrin-like and metallopeptidase (reprolysin type) with	Adamts10	0.000179221	2.95117
---		0.004088	2.95178
NM_009644 // Ahrr // aryl-hydrocarbon receptor repressor // 13 C2|13 // 11624 /// XM_00	Ahrr	5.16E-05	2.95687
NM_001077353 // Gsta3 // glutathione S-transferase, alpha 3 // 1 A4|1 6.5 cM // 14859 /	Gsta3	0.000694357	2.96018
NM_019986 // Habp4 // hyaluronic acid binding protein 4 // 13 B3|13 33.26 cM // 56541 /	Habp4	6.61E-06	2.9605
NM_029999 // Lbh // limb-bud and heart // 17 E2|17 // 77889 /// ENSMUST00000024857 // L	Lbh	7.44E-07	2.96453
NM_001033164 // 2510002D24Rik // RIKEN cDNA 2510002D24 gene // 16 A3|16 // 72307 /// EN	2510002D24Rik	0.000944933	2.96579
NM_001102471 // Cnnm2 // cyclin M2 // 19 C3|19 38.97 cM // 94219 /// NM_033569 // Cnnm2	Cnnm2	0.000205696	2.96666
XM_006513183 // Cradd // CASP2 and RIPK1 domain containing adaptor with death domain //	Cradd	4.82E-06	2.97087
NM_008979 // Ptpn22 // protein tyrosine phosphatase, non-receptor type 22 (lymphoid) //	Ptpn22	2.82E-07	2.9715
---		0.000393905	2.97445
---		4.72E-05	2.98173
NM_001033385 // Tbc1d32 // TBC1 domain family, member 32 // 10 B3|10 // 544696 /// ENSM	Tbc1d32	2.10E-05	2.9824
NM_001008542 // Mxi1 // Max interacting protein 1 // 19 D|19 47.53 cM // 17859 /// NM_0	Mxi1	7.63E-09	2.98338
NM_001166493 // Rasgrp3 // RAS, guanyl releasing protein 3 // 17 E2|17 // 240168 /// NM	Rasgrp3	1.07E-06	2.99087
NM_027288 // Manba // mannosidase, beta A, lysosomal // 3 H2|3 62.65 cM // 110173 /// E	Manba	2.43E-07	2.99117
NR_045696 // 9330133O14Rik // RIKEN cDNA 9330133O14 gene // 8 E1 // 100689703	9330133O14Rik	4.81E-05	2.99465
NM_144804 // Depdc7 // DEP domain containing 7 // 2 E2|2 // 211896 /// ENSMUST000000285	Depdc7	8.88E-06	3.00235
NM_001178012 // Sfxn3 // sideroflexin 3 // 19|19 D1 // 94280 /// NM_001178013 // Sfxn3	Sfxn3	4.45E-06	3.00597
ENSMUST00000148876 // Mettl8 // methyltransferase like 8 // 2 C2|2 // 228019 /// NM_001	Mettl8	4.81E-05	3.00854
NM_001044744 // Gcdh // glutaryl-Coenzyme A dehydrogenase // 8 C3|8 41.28 cM // 270076	Gcdh	3.37E-09	3.01073
ENSMUST00000000896 // Pxmp4 // peroxisomal membrane protein 4 // 2|2 H2 // 59038 /// NM	Pxmp4	1.69E-06	3.0183
NM_001276455 // Slc19a2 // solute carrier family 19 (thiamine transporter), member 2 //	Slc19a2	3.01E-07	3.01955
NM_001047604 // Ttc21b // tetratricopeptide repeat domain 21B // 2 C1.3|2 // 73668 ///	Ttc21b	0.000238114	3.0214
NM_009029 // Rb1 // retinoblastoma 1 // 14 D3|14 38.73 cM // 19645 /// XR_383150 // Rb1	Rb1	1.81E-07	3.0228
NM_177683 // Vgll4 // vestigial like 4 (Drosophila) // 6 E3|6 // 232334 /// XM_00650601	Vgll4	2.63E-05	3.02417
NM_001293637 // Nek1 // NIMA (never in mitosis gene a)-related expressed kinase 1 // 8	Nek1	0.000171816	3.03282
NM_026916 // Nupr1l // nuclear protein transcriptional regulator 1 like // 5|5 // 69034	Nupr1l	6.53E-06	3.03377
NM_009577 // Zik1 // zinc finger protein interacting with K protein 1 // 7 A1|7 // 2277	Zik1	0.00186189	3.03812
NM_001004062 // Crtc1 // CREB regulated transcription coactivator 1 // 8 B3.3|8 // 3820	Crtc1	1.57E-07	3.03818
NM_153571 // Hscb // HscB iron-sulfur cluster co-chaperone homolog (E. coli) // 5 F|5 /	Hscb	9.07E-06	3.03991
---		0.00368352	3.042
NM_001159559 // Xrcc6bp1 // XRCC6 binding protein 1 // 10 D3|10 // 68876 /// ENSMUST000	Xrcc6bp1	0.000218516	3.04519
---		0.000300899	3.04668
NM_008924 // Prkar2a // protein kinase, cAMP dependent regulatory, type II alpha // 9 F	Prkar2a	4.33E-07	3.04781
NM_001081259 // Mfsd7b // major facilitator superfamily domain containing 7B // 1 H6|1	Mfsd7b	1.51E-07	3.04977
NR_029535 // Mir99a // microRNA 99a // 16|16 // 387229 /// ENSMUST00000083596 // Mir99a	Mir99a	0.000776735	3.05059
NM_001004362 // 2610008E11Rik // RIKEN cDNA 2610008E11 gene // 10 C1|10 // 72128 /// EN	2610008E11Rik	0.000392035	3.05648
NM_010511 // Ifngr1 // interferon gamma receptor 1 // 10 A3|10 8.49 cM // 15979 /// ENS	Ifngr1	7.19E-06	3.05677
NM_001038703 // Gpr146 // G protein-coupled receptor 146 // 5|5 G1 // 80290 /// ENSMUST	Gpr146	2.26E-05	3.05682
NM_172573 // Engase // endo-beta-N-acetylglucosaminidase // 11 E2|11 // 217364 /// ENSM	Engase	0.000109172	3.06647
NM_001162375 // Fam73a // family with sequence similarity 73, member A // 3 H3|3 // 215	Fam73a	6.44E-05	3.06746
NM_153177 // Ago4 // argonaute RISC catalytic subunit 4 // 4 D2.2|4 // 76850 /// ENSMUS	Ago4	0.00160879	3.07145
NM_001290633 // Reps2 // RALBP1 associated Eps domain containing protein 2 // X F4|X //	Reps2	1.22E-06	3.07448
NM_020332 // Ank // progressive ankylosis // 15 B1|15 10.23 cM // 11732 /// ENSMUST0000	Ank	6.30E-07	3.07986
NM_010830 // Msh6 // mutS homolog 6 (E. coli) // 17 E4|17 57.87 cM // 17688 /// ENSMUST	Msh6	1.52E-05	3.08029
NM_025464 // Tmem218 // transmembrane protein 218 // 9 A4|9 // 66279 /// XM_006510545 /	Tmem218	2.43E-05	3.08186
NM_001289589 // Zfp12 // zinc finger protein 12 // 5 G2|5 // 231866 /// NM_001289590 //	Zfp12	1.39E-05	3.08548
NM_019426 // Atf7ip // activating transcription factor 7 interacting protein // 6 G1|6	Atf7ip	5.43E-08	3.08726
NM_001081266 // Ccdc142 // coiled-coil domain containing 142 // 6 C3|6 // 243510 /// EN	Ccdc142	0.000253712	3.08816
ENSMUST00000157170 // Gm25965 // predicted gene, 25965 // --- // ---	Gm25965	0.00142263	3.09083
---		0.00294985	3.09435
NM_019811 // Acss2 // acyl-CoA synthetase short-chain family member 2 // 2|2 H2 // 6052	Acss2	7.97E-08	3.09747
NM_175331 // Nt5dc3 // 5-nucleotidase domain containing 3 // 10 C1|10 // 103466 /// ENS	Nt5dc3	2.10E-06	3.09788
NR_015524 // Cep83os // centrosomal protein 83, opposite strand // 10 C2|10 // 67723 //	Cep83os	0.00203811	3.09922

NM_175511 // Fam78a // family with sequence similarity 78, member A // 2 B|2 // 241303	Fam78a	2.39E-05	3.10006
NM_027629 // Pgm2l1 // phosphoglucomutase 2-like 1 // 7|7 F1 // 70974 /// XM_006508205	Pgm2l1	3.70E-07	3.10183
NM_007671 // Cdkn2c // cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) // 4 C	Cdkn2c	0.000401537	3.10631
NM_028469 // 3110082I17Rik // RIKEN cDNA 3110082I17 gene // 5 G2|5 // 73212 /// XM_0065	3110082I17Rik	3.52E-05	3.11227
NM_030229 // Polr3h // polymerase (RNA) III (DNA directed) polypeptide H // 15|15 E2 //	Polr3h	0.00074933	3.11568
NR_001461 // Kcnq1ot1 // KCNQ1 overlapping transcript 1 // 7 F5|7 88.15 cM // 63830	Kcnq1ot1	0.00344788	3.12272
NM_010121 // Eif2ak3 // eukaryotic translation initiation factor 2 alpha kinase 3 // 6	Eif2ak3	8.38E-06	3.12411
NM_172694 // Megf9 // multiple EGF-like-domains 9 // 4 C2|4 // 230316 /// ENSMUST000001	Megf9	2.84E-06	3.12498
NM_001115130 // Zbtb44 // zinc finger and BTB domain containing 44 // 9 A4|9 // 235132	Zbtb44	1.03E-06	3.13115
ENSMUST00000134311 // Fos // FBJ osteosarcoma oncogene // 12 D2|12 39.7 cM // 14281 ///	Fos	1.66E-08	3.13186
NM_181071 // Tanc2 // tetratricopeptide repeat, ankyrin repeat and coiled-coil containi	Tanc2	7.79E-07	3.13339
NM_199308 // Mast3 // microtubule associated serine/threonine kinase 3 // 8 B3.3|8 // 5	Mast3	0.000550939	3.1399
NM_001195088 // Tmc8 // transmembrane channel-like gene family 8 // 11 E2|11 // 217356	Tmc8	1.99E-06	3.14368
NM_145460 // Oxnad1 // oxidoreductase NAD-binding domain containing 1 // 14 B|14 // 218	Oxnad1	0.000165483	3.14568
NM_001170489 // Aplf // aprataxin and PNKP like factor // 6 D1|6 // 72103 /// NM_024251	Aplf	8.55E-06	3.14718
NM_198105 // Fam120c // family with sequence similarity 120, member C // X|X F2 // 2073	Fam120c	6.35E-06	3.15098
---		0.00396231	3.15541
NM_008079 // Galc // galactosylceramidase // 12 E|12 49.83 cM // 14420 /// ENSMUST00000	Galc	9.75E-06	3.15741
NM_133218 // Zfp704 // zinc finger protein 704 // 3 A1|3 // 170753 /// ENSMUST000000411	Zfp704	1.46E-06	3.16354
NM_001128606 // Epb4.1 // erythrocyte protein band 4.1 // 4 D2.3|4 64.54 cM // 269587 /	Epb4.1	0.000122362	3.16496
NM_026543 // 3010026O09Rik // RIKEN cDNA 3010026O09 gene // 11 B1.3|11 // 68067 /// ENS	3010026O09Rik	0.000413827	3.16855
NM_139232 // Fgd4 // FYVE, RhoGEF and PH domain containing 4 // 16 A3|16 // 224014 ///	Fgd4	2.42E-06	3.1775
NM_026065 // Mrpl42 // mitochondrial ribosomal protein L42 // 10 C2|10 49.39 cM // 6727	Mrpl42	0.000874324	3.18786
NM_008131 // Glul // glutamate-ammonia ligase (glutamine synthetase) // 1 G2|1 // 14645	Glul	6.42E-08	3.2017
NM_001290784 // Ldlrad3 // low density lipoprotein receptor class A domain containing 3	Ldlrad3	3.08E-05	3.21227
NM_025969 // Timm21 // tranlocase of inner mitochondrial membrane 21 // 18|18 E3 // 671	Timm21	0.000148724	3.21331
NM_008841 // Pik3r2 // phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2	Pik3r2	8.21E-06	3.21521
NM_133185 // Rogdi // rogdi homolog (Drosophila) // 16 A1|16 2.49 cM // 66049 /// XM_00	Rogdi	1.93E-05	3.2154
NM_001030293 // Spry3 // sprouty homolog 3 (Drosophila) // --- // 236576 /// ENSMUST000	Spry3	2.84E-06	3.21642
NM_009531 // Xpc // xeroderma pigmentosum, complementation group C // 6|6 D // 22591 //	Xpc	1.62E-08	3.21876
NM_133931 // Pot1a // protection of telomeres 1A // 6 A3.1|6 // 101185 /// ENSMUST00000	Pot1a	3.12E-05	3.22246
NM_172779 // Ddx26b // DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B // X A5|X // 23	Ddx26b	5.79E-05	3.22247
NM_001177625 // Ect2 // ect2 oncogene // 3|3 B // 13605 /// NM_001177626 // Ect2 // ect	Ect2	2.18E-05	3.22799
NM_172926 // Snx14 // sorting nexin 14 // 9 E3.1|9 // 244962 /// XM_006511181 // Snx14	Snx14	3.21E-06	3.2282
NM_023645 // Kdelc1 // KDEL (Lys-Asp-Glu-Leu) containing 1 // 1|1 C1 // 72050 /// XM_00	Kdelc1	8.13E-07	3.22958
NM_178253 // Klhdc1 // kelch domain containing 1 // 12 C2|12 // 271005 /// XM_006515928	Klhdc1	0.000310588	3.23016
NM_007642 // Cd28 // CD28 antigen // 1 C1-C3|1 30.52 cM // 12487 /// ENSMUST00000027165	Cd28	2.76E-05	3.23055
NM_176996 // Smo // smoothened homolog (Drosophila) // 6 A3.3|6 12.36 cM // 319757 ///	Smo	1.36E-05	3.23419
---		0.000173999	3.24272
NM_133829 // Mfsd6 // major facilitator superfamily domain containing 6 // 1 C1.1|1 //	Mfsd6	1.80E-06	3.26017
BC049272 // Kif18b // kinesin family member 18B // 11 E1|11 // 70218 /// NM_197959 // K	Kif18b	0.00154197	3.26132
NM_178113 // Ncapd3 // non-SMC condensin II complex, subunit D3 // 9 A4|9 // 78658 ///	Ncapd3	1.94E-07	3.26341
---		0.00171292	3.26408
NM_133667 // Pdk2 // pyruvate dehydrogenase kinase, isoenzyme 2 // 11 D|11 59.01 cM //	Pdk2	0.000140508	3.26552
NM_008152 // Gpr65 // G-protein coupled receptor 65 // 12 E|12 // 14744 /// ENSMUST0000	Gpr65	3.09E-08	3.2658
XM_006533512 // Slc22a4 // solute carrier family 22 (organic cation transporter), membe	Slc22a4	1.03E-06	3.26965
NR_030698 // A630066F11Rik // RIKEN cDNA A630066F11 gene // 10|10 // 320642	A630066F11Rik	0.00239758	3.27053
NM_008517 // Lta4h // leukotriene A4 hydrolase // 10|10 C3 // 16993 /// ENSMUST00000016	Lta4h	1.33E-05	3.27174
NM_027289 // Nt5dc2 // 5-nucleotidase domain containing 2 // 14 B|14 // 70021 /// ENSMU	Nt5dc2	2.65E-07	3.27272
NM_001199283 // Slc43a2 // solute carrier family 43, member 2 // 11 B5|11 // 215113 ///	Slc43a2	6.78E-07	3.27417
NM_011385 // Ski // ski sarcoma viral oncogene homolog (avian) // 4 E2|4 86.17 cM // 20	Ski	7.58E-06	3.27534
NM_026260 // Tctn3 // tectonic family member 3 // 19 C3|19 // 67590 /// ENSMUST00000025	Tctn3	1.15E-07	3.27995
NM_001293701 // Polr3gl // polymerase (RNA) III (DNA directed) polypeptide G like // 3	Polr3gl	1.43E-06	3.28026
NM_001081433 // Ankrd44 // ankyrin repeat domain 44 // 1 C1.1|1 // 329154 /// ENSMUST00	Ankrd44	2.08E-07	3.2861
NM_001162947 // Nek3 // NIMA (never in mitosis gene a)-related expressed kinase 3 // 8	Nek3	0.000103455	3.29166
NM_199475 // Fam63a // family with sequence similarity 63, member A // 3|3 F2 // 75007	Fam63a	4.11E-07	3.29294
NM_001290790 // Plcb2 // phospholipase C, beta 2 // 2 E5|2 59.43 cM // 18796 /// NM_177	Plcb2	5.50E-08	3.29899
NM_201609 // Zfp652 // zinc finger protein 652 // 11 D|11 // 268469 /// ENSMUST00000091	Zfp652	1.76E-06	3.29936
NM_018822 // Sgsh // N-sulfoglucosamine sulfohydrolase (sulfamidase) // 11 E2|11 83.36	Sgsh	3.97E-07	3.29967
NM_183390 // Klhl6 // kelch-like 6 // 16 A3|16 // 239743 /// ENSMUST00000058839 // Klhl	Klhl6	1.28E-05	3.30489
NM_146008 // Tcp11l2 // t-complex 11 (mouse) like 2 // 10 C1|10 // 216198 /// ENSMUST00	Tcp11l2	0.000352699	3.30583
NM_144812 // Tnrc6b // trinucleotide repeat containing 6b // 15 E1|15 // 213988 /// NM_	Tnrc6b	2.77E-05	3.30993
---		5.92E-05	3.31122
NM_029654 // Atg2b // autophagy related 2B // 12 E|12 // 76559 /// ENSMUST00000041055 /	Atg2b	1.96E-05	3.31361
---		0.00530807	3.3194
NM_001285785 // Arhgap9 // Rho GTPase activating protein 9 // 10 D3|10 // 216445 /// NM	Arhgap9	6.70E-07	3.32167
NM_001004363 // Nuak1 // NUAK family, SNF1-like kinase, 1 // 10 C1|10 // 77976 /// ENSM	Nuak1	0.00140047	3.32257
NM_001026214 // Entpd5 // ectonucleoside triphosphate diphosphohydrolase 5 // 12 E|12 3	Entpd5	7.57E-08	3.32287
ENSMUST00000126677 // Gm15537 // predicted gene 15537 // --- // ---	Gm15537	4.42E-06	3.32418
NM_001033352 // Klhl21 // kelch-like 21 // 4 E2|4 // 242785 /// ENSMUST00000097773 // K	Klhl21	0.00013531	3.32954
NM_019800 // Acp6 // acid phosphatase 6, lysophosphatidic // 3 F2.1|3 // 66659 /// XR_3	Acp6	3.62E-05	3.32989
NM_009469 // Ulk1 // unc-51 like kinase 1 // 5|5 F // 22241 /// ENSMUST00000031490 // U	Ulk1	2.62E-06	3.34077
NM_172465 // Zdhhc9 // zinc finger, DHHC domain containing 9 // X A4|X // 208884 /// EN	Zdhhc9	1.25E-07	3.34102
NM_011937 // Gnpda1 // glucosamine-6-phosphate deaminase 1 // 18 B3|18 // 26384 /// ENS	Gnpda1	7.23E-07	3.34973
NM_001033167 // Slc22a23 // solute carrier family 22, member 23 // 13 A3.3|13 // 73102	Slc22a23	2.70E-05	3.35348
NM_015786 // Hist1h1c // histone cluster 1, H1c // 13|13 A2-A3 // 50708 /// ENSMUST0000	Hist1h1c	6.36E-07	3.35635
NM_001039511 // Ivns1abp // influenza virus NS1A binding protein // 1 G2|1 // 117198 //	Ivns1abp	4.71E-07	3.35666
NM_001164598 // Irf2bp2 // interferon regulatory factor 2 binding protein 2 // 8 E2|8 /	Irf2bp2	1.30E-07	3.37045
---		0.00110064	3.38071
NM_177184 // Vps13c // vacuolar protein sorting 13C (yeast) // 9 C|9 // 320528 /// ENSM	Vps13c	3.47E-07	3.38381
NM_019740 // Foxo3 // forkhead box O3 // 10 B2|10 22.79 cM // 56484 /// XR_380270 // LO	Foxo3	1.28E-06	3.38702
NM_133792 // Pla2g15 // phospholipase A2, group XV // 8 D3|8 // 192654 /// ENSMUST00000	Pla2g15	4.62E-08	3.38716
NM_001163042 // Haus8 // 4HAUS augmin-like complex, subunit 8 // 8|8 C1 // 76478 /// NM	Haus8	4.30E-05	3.39872
NM_029436 // Klhl24 // kelch-like 24 // 16|16 B1 // 75785 /// ENSMUST00000023509 // Klh	Klhl24	2.18E-05	3.40123
NM_026192 // Calcoco1 // calcium binding and coiled coil domain 1 // 15 F3|15 // 67488	Calcoco1	7.48E-08	3.402
NM_145588 // Kif22 // kinesin family member 22 // 7 F3|7 69.29 cM // 110033 /// ENSMUST	Kif22	4.76E-05	3.42486
---		0.00157777	3.42734
NM_029938 // H2afv // H2A histone family, member V // 11 A1|11 // 77605 /// ENSMUST0000	H2afv	1.30E-05	3.43182
NM_001198789 // Ccpg1os // cell cycle progression 1, opposite strand // 9 D|9 // 546143	Ccpg1os	1.63E-08	3.4405

NM_010568 // Insr // insulin receptor // 8 A1.1|8 1.82 cM // 16337 /// ENSMUST000000912	Insr	5.35E-06	3.44153
NM_198308 // Pdpr // pyruvate dehydrogenase phosphatase regulatory subunit // 8 E1|8 //	Pdpr	2.70E-06	3.44322
NM_175445 // Rassf2 // Ras association (RalGDS/AF-6) domain family member 2 // 2 F2|2 /	Rassf2	7.03E-08	3.44838
NM_001252094 // Mettl20 // methyltransferase like 20 // 6 G3|6 // 320204 /// NM_0012520	Mettl20	0.000398718	3.47501
NM_028149 // Fbxl20 // F-box and leucine-rich repeat protein 20 // 11 D|11 // 72194 ///	Fbxl20	1.41E-06	3.48401
NM_138745 // Mthfd1 // methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methe	Mthfd1	1.27E-05	3.48645
NM_011906 // Tpra1 // transmembrane protein, adipocyte asscociated 1 // 6|6 D2 // 24100	Tpra1	4.84E-07	3.48998
NM_001184706 // Tfdp2 // transcription factor Dp 2 // 9 E3.3|9 // 211586 /// NM_0011847	Tfdp2	5.54E-05	3.49539
NM_009213 // Smpd2 // sphingomyelin phosphodiesterase 2, neutral // 10 B2|10 // 20598 /	Smpd2	7.75E-05	3.50305
NM_001080746 // Gtf2i // general transcription factor II I // 5 G2|5 74.48 cM // 14886	Gtf2i	2.33E-05	3.50432
NM_009274 // Srpk2 // serine/arginine-rich protein specific kinase 2 // 5 A3|5 10.36 cM	Srpk2	5.39E-07	3.5044
NM_010497 // Idh1 // isocitrate dehydrogenase 1 (NADP+), soluble // 1 C2|1 32.91 cM //	Idh1	2.22E-08	3.517
---		0.00593002	3.519
---		0.00485474	3.52122
NM_001163495 // Arhgap19 // Rho GTPase activating protein 19 // 19|19 D1 // 71085 /// N	Arhgap19	0.00010112	3.52632
NM_183276 // Nbeal2 // neurobeachin-like 2 // 9 F2|9 // 235627 /// ENSMUST00000133191 /	Nbeal2	1.66E-07	3.52737
NM_001163378 // 2700049A03Rik // RIKEN cDNA 2700049A03 gene // 12|12 C3 // 76967 /// NM	2700049A03Rik	8.07E-07	3.53809
NM_029645 // Gatc // glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	Gatc	0.000102617	3.54044
NM_177372 // Dna2 // DNA replication helicase 2 homolog (yeast) // 10 B4|10 // 327762 /	Dna2	1.40E-07	3.5477
NM_199197 // Rbfa // ribosome binding factor A // 18 E3|18 // 68731 /// ENSMUST00000025	Rbfa	0.000206571	3.55152
AK159040 // 9130004J05Rik // RIKEN cDNA 9130004J05 gene // 15|15 // 71603	9130004J05Rik	0.00211247	3.56515
---		0.00630464	3.56993
NM_207161 // Dnph1 // 2-deoxynucleoside 5-phosphate N-hydrolase 1 // 17 C|17 // 381101	Dnph1	0.000575852	3.58524
NM_026599 // Cgnl1 // cingulin-like 1 // 9 D|9 // 68178 /// XM_006511395 // Cgnl1 // ci	Cgnl1	4.72E-06	3.59088
NM_031251 // Ctns // cystinosis, nephropathic // 11 B4|11 // 83429 /// XM_006534533 //	Ctns	3.86E-07	3.59779
NM_028048 // Slc25a35 // solute carrier family 25, member 35 // 11 B3|11 // 71998 /// E	Slc25a35	7.18E-06	3.60054
NM_001291190 // Ssh2 // slingshot homolog 2 (Drosophila) // 11 B5|11 // 237860 /// NM_1	Ssh2	8.34E-08	3.60084
NM_153804 // Plekhg3 // pleckstrin homology domain containing, family G (with RhoGef do	Plekhg3	6.81E-07	3.60759
NM_001190320 // Clec4n // C-type lectin domain family 4, member n // 6 F3|6 58.3 cM //	Clec4n	1.08E-07	3.61421
NR_102275 // AI839979 // expressed sequence AI839979 // --- // 100740	AI839979	0.000995154	3.63358
---		1.48E-05	3.64526
NR_037959 // 1600010M07Rik // RIKEN cDNA 1600010M07 gene // 7|7 // 69781 /// AK005418 /	1600010M07Rik	0.000365558	3.64917
NM_025449 // Nicn1 // nicolin 1 // 9 F2|9 // 66257 /// ENSMUST00000035227 // Nicn1 // n	Nicn1	9.66E-07	3.65175
NM_001077696 // Hdac5 // histone deacetylase 5 // 11 D|11 // 15184 /// NM_001284248 //	Hdac5	5.14E-07	3.65762
XM_006506475 // Fam136a // family with sequence similarity 136, member A // 6 D1|6 // 6	Fam136a	0.000186046	3.66125
ENSMUST00000075588 // Tnfrsf22 // tumor necrosis factor receptor superfamily, member 22	Tnfrsf22	0.000676646	3.67683
NM_175337 // Mlh3 // mutL homolog 3 (E coli) // 12 D2|12 // 217716 /// ENSMUST000000193	Mlh3	0.000263422	3.67724
NM_025807 // Slc16a9 // solute carrier family 16 (monocarboxylic acid transporters), me	Slc16a9	2.51E-05	3.68395
NM_174987 // Coa6 // cytochrome c oxidase assembly factor 6 // 8 E2|8 // 67892 /// ENSM	Coa6	0.000359279	3.69077
NM_026272 // Narf // nuclear prelamin A recognition factor // 11 E2|11 // 67608 /// ENS	Narf	6.06E-06	3.69179
---		0.000664722	3.69439
---		0.00145151	3.70204
NM_001167832 // Zfp764 // zinc finger protein 764 // 7 F3|7 // 233893 /// NM_146203 //	Zfp764	4.41E-05	3.71639
NR_046157 // Gm5086 // predicted gene 5086 // 13 D1|13 // 328314	Gm5086	5.40E-05	3.71742
NM_024245 // Kif23 // kinesin family member 23 // 9 B|9 // 71819 /// ENSMUST00000034815	Kif23	0.00034265	3.74697
NM_027534 // Kdsr // 3-ketodihydrosphingosine reductase // 1 E2.1|1 // 70750 /// XM_006	Kdsr	6.58E-06	3.75994
NM_008856 // Prkch // protein kinase C, eta // 12|12 C3-D1 // 18755 /// ENSMUST00000021	Prkch	4.32E-07	3.7647
NM_028995 // Nipal3 // NIPA-like domain containing 3 // 4 D3|4 // 74552 /// XM_00653922	Nipal3	1.06E-07	3.76616
NM_197987 // Trim37 // tripartite motif-containing 37 // 11 C|11 // 68729 /// ENSMUST00	Trim37	6.71E-06	3.78131
NM_008425 // Kcnj2 // potassium inwardly-rectifying channel, subfamily J, member 2 // 1	Kcnj2	0.000111591	3.78302
NR_002864 // Peg13 // paternally expressed 13 // 15 D3|15 // 353342	Peg13	7.82E-07	3.7875
NM_172693 // Galnt12 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactos	Galnt12	0.0030931	3.80669
NM_175128 // 4930430F08Rik // RIKEN cDNA 4930430F08 gene // 10 D1|10 // 68281 /// ENSMU	4930430F08Rik	0.00123909	3.80695
NM_001163608 // Plxdc1 // plexin domain containing 1 // 11 D|11 // 72324 /// NM_028199	Plxdc1	2.50E-07	3.81808
NM_019975 // Hacl1 // 2-hydroxyacyl-CoA lyase 1 // 14 B|14 // 56794 /// XM_006519320 //	Hacl1	1.03E-06	3.82278
NM_001083341 // Mboat2 // membrane bound O-acyltransferase domain containing 2 // 12 A1	Mboat2	0.000644177	3.83901
---		0.000984989	3.84583
NM_027909 // C2cd2l // C2 calcium-dependent domain containing 2-like // 9|9 B // 71764	C2cd2l	6.46E-06	3.85243
NM_011133 // Pole2 // polymerase (DNA directed), epsilon 2 (p59 subunit) // 12|12 C3 //	Pole2	2.60E-07	3.87159
NM_020270 // Scamp5 // secretory carrier membrane protein 5 // 9 B|9 // 56807 /// XM_00	Scamp5	9.52E-06	3.87484
NM_016681 // Chek2 // checkpoint kinase 2 // 5 F|5 // 50883 /// XM_006535068 // Chek2 /	Chek2	2.30E-06	3.87961
NM_172681 // D930015E06Rik // RIKEN cDNA D930015E06 gene // 3 F1|3 // 229473 /// ENSMUS	D930015E06Rik	1.90E-06	3.89911
NM_001033393 // Tmem104 // transmembrane protein 104 // 11 E2|11 // 320534 /// ENSMUST0	Tmem104	2.91E-06	3.90125
ENSMUST00000086363 // Tmem150b // transmembrane protein 150B // 7 A1|7 // 330460 /// NM	Tmem150b	1.01E-05	3.9061
NM_001164099 // Add3 // adducin 3 (gamma) // 19 D2|19 47.18 cM // 27360 /// NM_00116410	Add3	1.98E-05	3.91505
NM_170758 // Cd300a // CD300A antigen // 11 E2|11 80.54 cM // 217303 /// XM_006533069 /	Cd300a	5.15E-07	3.92312
NM_001113283 // Fam214a // family with sequence similarity 214, member A // 9 D|9 // 23	Fam214a	7.32E-08	3.92481
NM_153542 // Lrrc20 // leucine rich repeat containing 20 // 10 B4|10 // 216011 /// ENSM	Lrrc20	1.30E-07	3.92634
NM_052976 // Ophn1 // oligophrenin 1 // X|X C2 // 94190 /// ENSMUST00000033560 // Ophn1	Ophn1	4.71E-08	3.92734
NM_001163760 // 6430548M08Rik // RIKEN cDNA 6430548M08 gene // 8 E1|8 // 234797 /// NM_	6430548M08Rik	1.58E-06	3.92969
NM_146094 // Fads1 // fatty acid desaturase 1 // 19 A|19 // 76267 /// ENSMUST0000001080	Fads1	2.30E-10	3.93208
NM_010658 // Mafb // v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (	Mafb	1.06E-08	3.93776
NM_145475 // Cerk // ceramide kinase // 15 E2|15 // 223753 /// ENSMUST00000044332 // Ce	Cerk	5.32E-08	3.95543
NM_001145960 // Slc37a2 // solute carrier family 37 (glycerol-3-phosphate transporter),	Slc37a2	1.51E-07	3.96226
NM_028894 // Lonrf3 // LON peptidase N-terminal domain and ring finger 3 // X|X A2 // 7	Lonrf3	2.13E-06	3.98212
---		0.00276685	4.00083
---		0.000521207	4.00732
NM_001001806 // Zfp36l2 // zinc finger protein 36, C3H type-like 2 // 17 E4|17 // 12193	Zfp36l2	3.50E-08	4.01703
---		0.00206897	4.0495
NM_020567 // Gmnn // geminin // 13 A3.1|13 // 57441 /// XM_006516722 // Gmnn // geminin	Gmnn	3.28E-05	4.05904
NM_001081128 // Mtr // 5-methyltetrahydrofolate-homocysteine methyltransferase // 13 A1	Mtr	2.14E-05	4.06568
NM_172134 // Pdxk // pyridoxal (pyridoxine, vitamin B6) kinase // 10 C1|10 39.72 cM //	Pdxk	4.06E-07	4.06933
NM_024184 // Asf1b // anti-silencing function 1B histone chaperone // 8 C3|8 // 66929 /	Asf1b	0.00109549	4.08832
NM_001142701 // Hmha1 // histocompatibility (minor) HA-1 // 10 C1|10 // 70719 /// NM_02	Hmha1	4.66E-07	4.08964
---		0.00560658	4.1452
NM_133765 // Fbxo31 // F-box protein 31 // 8 E1|8 // 76454 /// ENSMUST00000059018 // Fb	Fbxo31	6.84E-07	4.16675
NM_001289895 // Tns1 // tensin 1 // 1 C3|1 38.17 cM // 21961 /// NM_027884 // Tns1 // t	Tns1	7.06E-08	4.17112
NM_016974 // Dbp // D site albumin promoter binding protein // 7 B4|7 29.45 cM // 13170	Dbp	1.51E-05	4.18229
NM_173442 // Gcnt1 // glucosaminyl (N-acetyl) transferase 1, core 2 // 19 B|19 12.75 cM	Gcnt1	3.05E-06	4.18656

NM_001079686 // Syne1 // spectrin repeat containing, nuclear envelope 1 // 10 A1|10 //	Syne1	1.91E-05	4.19033
NM_018789 // Foxo4 // forkhead box O4 // X C3-D|X 43.89 cM // 54601 /// ENSMUST00000062	Foxo4	0.00140243	4.19144
NM_178589 // Tnfrsf21 // tumor necrosis factor receptor superfamily, member 21 // 17|17	Tnfrsf21	6.53E-09	4.202
NM_001276292 // Wwp1 // WW domain containing E3 ubiquitin protein ligase 1 // 4 A3|4 //	Wwp1	2.19E-09	4.22519
ENSMUST00000104480 // Gm26143 // predicted gene, 26143 // --- // ---	Gm26143	8.04E-06	4.23445
NM_146040 // Cdca7l // cell division cycle associated 7 like // 12 F2|12 // 217946 ///	Cdca7l	6.31E-05	4.25859
---		0.00171893	4.27098
NM_001081176 // Polr3g // polymerase (RNA) III (DNA directed) polypeptide G // 13 C3|13	Polr3g	3.05E-08	4.28052
---		7.81E-06	4.31809
NM_016917 // Slc40a1 // solute carrier family 40 (iron-regulated transporter), member 1	Slc40a1	6.34E-09	4.31818
---		0.00589373	4.3215
NM_008628 // Msh2 // mutS homolog 2 (E. coli) // 17 E4|17 57.87 cM // 17685 /// ENSMUST	Msh2	3.35E-05	4.33216
NM_028964 // Snx29 // sorting nexin 29 // --- // 74478 /// ENSMUST00000122168 // Snx29	Snx29	5.93E-05	4.35445
NM_012006 // Acot1 // acyl-CoA thioesterase 1 // 12 D1|12 39.0 cM // 26897 /// ENSMUST0	Acot1	0.000801152	4.36034
NM_001099738 // Dnajc28 // DnaJ (Hsp40) homolog, subfamily C, member 28 // 16 C3.3|16 /	Dnajc28	0.000138227	4.3736
NM_001081326 // Agl // amylo-1,6-glucosidase, 4-alpha-glucanotransferase // 3 G1|3 // 7	Agl	3.01E-05	4.37535
NM_172468 // Snx30 // sorting nexin family member 30 // 4 B3|4 // 209131 /// ENSMUST000	Snx30	2.42E-08	4.44061
NM_001161763 // Fmo5 // flavin containing monooxygenase 5 // 3 F2.2|3 // 14263 /// NM_0	Fmo5	3.45E-06	4.44519
NM_011159 // Prkdc // protein kinase, DNA activated, catalytic polypeptide // 16 10.09	Prkdc	6.59E-07	4.49516
---		0.000103766	4.51287
NM_001190297 // Gpr155 // G protein-coupled receptor 155 // 2 C3|2 // 68526 /// NM_0012	Gpr155	2.68E-05	4.52691
NM_001130412 // Lpin1 // lipin 1 // 12 A1.1|12 7.9 cM // 14245 /// NM_015763 // Lpin1 /	Lpin1	2.90E-05	4.56102
ENSMUST00000180988 // Gm26912 // predicted gene, 26912 // --- // ---	Gm26912	9.49E-05	4.5685
NM_001081396 // Tbc1d31 // TBC1 domain family, member 31 // 15 D1|15 // 210544 /// NM_0	Tbc1d31	6.20E-07	4.58111
NM_172771 // Dmxl2 // Dmx-like 2 // 9|9 C // 235380 /// ENSMUST00000118163 // Dmxl2 //	Dmxl2	3.97E-07	4.59891
NM_027491 // Rragd // Ras-related GTP binding D // 4 A5|4 14.57 cM // 52187 /// ENSMUST	Rragd	3.81E-06	4.60999
NM_029482 // 4930579G24Rik // RIKEN cDNA 4930579G24 gene // 3|3 F1 // 75939 /// ENSMUST	4930579G24Rik	0.000134984	4.61866
NM_177337 // Arl11 // ADP-ribosylation factor-like 11 // 14 D1|14 // 219144 /// XM_0065	Arl11	9.73E-08	4.62287
NM_021310 // Jmy // junction-mediating and regulatory protein // 13 C3|13 // 57748 ///	Jmy	9.69E-08	4.63693
---		0.000859953	4.65945
NM_175645 // Xylt1 // xylosyltransferase 1 // 7 F2|7 // 233781 /// ENSMUST00000032892 /	Xylt1	2.23E-06	4.67984
NM_028340 // Susd3 // sushi domain containing 3 // 13|13 B1 // 66329 /// XM_006516941 /	Susd3	5.93E-05	4.68245
NM_001005341 // Ypel2 // yippee-like 2 (Drosophila) // 11 C|11 // 77864 /// ENSMUST0000	Ypel2	5.05E-06	4.7203
NM_009025 // Rasa3 // RAS p21 protein activator 3 // 8 A1.1|8 6.29 cM // 19414 /// XM_0	Rasa3	1.44E-07	4.73008
NM_145938 // Rpp40 // ribonuclease P 40 subunit // 13 A3.3|13 // 208366 /// XM_00651663	Rpp40	0.000108259	4.73663
NM_183031 // Gpr183 // G protein-coupled receptor 183 // 14 E5|14 // 321019 /// ENSMUST	Gpr183	2.36E-07	4.74425
NM_001163268 // Lpar5 // lysophosphatidic acid receptor 5 // 6 F2|6 // 381810 /// ENSMU	Lpar5	0.000494173	4.75517
NM_029091 // Klc4 // kinesin light chain 4 // 17 C|17 // 74764 /// XM_006525042 // Klc4	Klc4	9.95E-06	4.79101
NM_134188 // Acot2 // acyl-CoA thioesterase 2 // 12|12 D3 // 171210 /// ENSMUST00000021	Acot2	7.76E-06	4.81287
NM_001170694 // Rcbtb2 // regulator of chromosome condensation (RCC1) and BTB (POZ) dom	Rcbtb2	4.36E-07	4.83057
NM_146073 // Zdhhc14 // zinc finger, DHHC domain containing 14 // 17 A1|17 // 224454 //	Zdhhc14	2.30E-07	4.83978
NM_133898 // N4bp2l1 // NEDD4 binding protein 2-like 1 // 5 G3|5 // 100637 /// ENSMUST0	N4bp2l1	9.55E-07	4.84271
---		0.00250987	4.84813
---		0.00648934	4.88267
XM_006527412 // Rab3il1 // RAB3A interacting protein (rabin3)-like 1 // 19 A|19 // 7476	Rab3il1	4.10E-08	4.88372
---		0.00255325	4.88429
NM_181401 // Tmem64 // transmembrane protein 64 // 4 A2|4 // 100201 /// ENSMUST00000062	Tmem64	1.48E-07	4.88689
NM_001270537 // Bin2 // bridging integrator 2 // 15 F1|15 // 668218 /// ENSMUST00000182	Bin2	6.31E-07	4.8884
---		9.67E-06	4.89615
NM_177231 // Arrb1 // arrestin, beta 1 // 7 E2|7 54.09 cM // 109689 /// NM_178220 // Ar	Arrb1	5.13E-10	4.91596
NM_001042591 // Arrdc3 // arrestin domain containing 3 // 13 C3|13 // 105171 /// XM_006	Arrdc3	5.52E-09	4.93264
NM_008115 // Gfra2 // glial cell line derived neurotrophic factor family receptor alpha	Gfra2	5.13E-07	4.94602
NM_028372 // Mblac2 // metallo-beta-lactamase domain containing 2 // 13 C3|13 // 72852	Mblac2	9.91E-08	4.99099
---		0.00660571	4.99192
NM_030251 // Abtb1 // ankyrin repeat and BTB (POZ) domain containing 1 // 6 D1|6 // 802	Abtb1	8.50E-07	4.99214
NM_145220 // Appl2 // adaptor protein, phosphotyrosine interaction, PH domain and leuci	Appl2	9.50E-07	5.00186
NM_027872 // Slc46a3 // solute carrier family 46, member 3 // 5 G3|5 // 71706 /// XM_00	Slc46a3	2.17E-07	5.01576
NM_033602 // Peli2 // pellino 2 // 14 C1|14 24.6 cM // 93834 /// XM_006519740 // Peli2	Peli2	2.48E-06	5.0211
---		0.000858014	5.02348
NM_009128 // Scd2 // stearoyl-Coenzyme A desaturase 2 // 19 C3|19 37.98 cM // 20250 ///	Scd2	7.40E-11	5.04277
---		0.00298249	5.05527
---		0.00298692	5.06922
NM_177000 // C130050O18Rik // RIKEN cDNA C130050O18 gene // 5 G2|5 // 319772 /// ENSMUS	C130050O18Rik	0.00023376	5.10769
NM_009987 // Cx3cr1 // chemokine (C-X3-C motif) receptor 1 // 9 F4|9 // 13051 /// ENSMU	Cx3cr1	1.45E-06	5.14486
ENSMUST00000083115 // Gm24041 // predicted gene, 24041 // --- // ---	Gm24041	0.000118076	5.15411
---		0.00465442	5.16962
NM_010753 // Mxd4 // Max dimerization protein 4 // 5 B2|5 17.84 cM // 17122 /// ENSMUST	Mxd4	3.32E-05	5.19344
NM_001168491 // Pdcd4 // programmed cell death 4 // 19 D2|19 48.73 cM // 18569 /// NM_0	Pdcd4	1.40E-06	5.19504
---		0.00396414	5.29807
NM_001289740 // Mturn // maturin, neural progenitor differentiation regulator homolog (	Mturn	2.18E-07	5.30842
---		0.00197267	5.32397
NM_176837 // Arhgap18 // Rho GTPase activating protein 18 // 10 A4|10 // 73910 /// XM_0	Arhgap18	3.01E-08	5.35785
NM_138956 // Rassf3 // Ras association (RalGDS/AF-6) domain family member 3 // 10 D2|10	Rassf3	2.36E-07	5.39814
NM_001033257 // Phactr2 // phosphatase and actin regulator 2 // 10 A2|10 // 215789 ///	Phactr2	2.64E-06	5.40635
NM_023326 // Bmyc // brain expressed myelocytomatosis oncogene // 2 A3|2 // 107771 ///	Bmyc	7.81E-06	5.4613
NM_145401 // Prkag2 // protein kinase, AMP-activated, gamma 2 non-catalytic subunit //	Prkag2	5.82E-08	5.46539
NM_145853 // Tpcn1 // two pore channel 1 // 5 F|5 // 252972 /// ENSMUST00000046426 // T	Tpcn1	0.00012439	5.46886
---		0.000482856	5.47171
NM_001199105 // Trp53inp1 // transformation related protein 53 inducible nuclear protei	Trp53inp1	2.60E-07	5.47272
ENSMUST00000150912 // Stard9 // START domain containing 9 // 2 E5|2 // 668880 /// ENSMU	Stard9	1.99E-07	5.53742
NM_172514 // Tmem71 // transmembrane protein 71 // 15 D2|15 // 213068 /// ENSMUST000000	Tmem71	7.69E-07	5.62653
---		0.00203752	5.66189
NM_018775 // Tbc1d8 // TBC1 domain family, member 8 // 1 B|1 // 54610 /// XM_006496146	Tbc1d8	3.96E-08	5.73607
---		0.00210668	5.77001
NM_001287514 // Cebpa // CCAAT/enhancer binding protein (C/EBP), alpha // 7 B1|7 21.02	Cebpa	6.24E-08	5.78863
---		4.38E-05	5.90715
---		0.00149403	6.02617
NM_001170643 // Rnf144b // ring finger protein 144B // 13 A5|13 // 218215 /// NM_146042	Rnf144b	2.15E-07	6.09794
NM_001271413 // Nfam1 // Nfat activating molecule with ITAM motif 1 // 15|15 E2 // 7403	Nfam1	9.53E-08	6.12583

NM_198664 // Tbc1d2 // TBC1 domain family, member 2 // 4 B1|4 // 381605 /// ENSMUST0000	Tbc1d2	6.30E-06	6.21982
NM_021462 // Mknk2 // MAP kinase-interacting serine/threonine kinase 2 // 10 C1|10 // 1	Mknk2	4.31E-07	6.24005
NM_026436 // Tmem86a // transmembrane protein 86A // 7 B4|7 // 67893 /// ENSMUST0000001	Tmem86a	7.76E-07	6.30914
NM_001146180 // Mtss1 // metastasis suppressor 1 // 15 D1|15 // 211401 /// NM_144800 //	Mtss1	6.98E-09	6.44171
---		6.51E-07	6.53994
NM_199221 // Cd300lb // CD300 antigen like family member B // 11 E2|11 // 217304 /// EN	Cd300lb	1.54E-09	6.60477
NR_030718 // F630028O10Rik // RIKEN cDNA F630028O10 gene // X C3|X // 100038363 /// ENS	F630028O10Rik	7.40E-07	6.63335
NM_009128 // Scd2 // stearoyl-Coenzyme A desaturase 2 // 19 C3|19 37.98 cM // 20250 ///	Scd2	1.40E-07	6.69929
---		0.00067707	6.89075
---		1.22E-06	6.89436
NM_001013370 // Sesn1 // sestrin 1 // 10 B2|10 22.77 cM // 140742 /// NM_001162908 // S	Sesn1	2.72E-07	6.90316
---		4.11E-05	6.93345
---		0.000974395	7.52172
NM_001242423 // Fam105a // family with sequence similarity 105, member A // 15 B1|15 //	Fam105a	1.04E-07	7.726
NM_026189 // Eepd1 // endonuclease/exonuclease/phosphatase family domain containing 1 /	Eepd1	1.60E-08	8.076
XM_006500510 // Stard9 // START domain containing 9 // 2 E5|2 // 668880 /// ENSMUST0000	Stard9	1.28E-07	8.30015
NM_175930 // Rapgef5 // Rap guanine nucleotide exchange factor (GEF) 5 // 12 F2|12 // 2	Rapgef5	1.35E-09	8.30471
NM_001252506 // St6gal1 // beta galactoside alpha 2,6 sialyltransferase 1 // 16 B1|16 1	St6gal1	8.62E-08	8.45208
NM_009924 // Cnr2 // cannabinoid receptor 2 (macrophage) // 4 D3|4 // 12802 /// ENSMUST	Cnr2	8.69E-07	8.47887
NM_008535 // Lyl1 // lymphoblastomic leukemia 1 // 8 C3|8 41.02 cM // 17095 /// ENSMUST	Lyl1	1.23E-07	8.69163
ENSMUST00000106357 // Ypel3 // yippee-like 3 (Drosophila) // 7 F3|7 // 66090 /// NM_025	Ypel3	5.99E-08	8.77434
---		0.000235818	8.90352
---		0.000594544	8.93783
ENSMUST00000170967 // Rb1 // retinoblastoma 1 // 14 D3|14 38.73 cM // 19645	Rb1	3.61E-06	9.18381
---		7.61E-06	10.3889
---		0.00512012	10.818
NM_175116 // Lpar6 // lysophosphatidic acid receptor 6 // 14 D3|14 // 67168 /// ENSMUST	Lpar6	5.68E-10	11.0058
---		3.69E-05	12.518
NM_001039484 // Kcnj10 // potassium inwardly-rectifying channel, subfamily J, member 10	Kcnj10	1.50E-06	13.4457
NM_009911 // Cxcr4 // chemokine (C-X-C motif) receptor 4 // 1 E4|1 56.43 cM // 12767 //	Cxcr4	2.50E-09	14.8111
NM_011994 // Abcd2 // ATP-binding cassette, sub-family D (ALD), member 2 // 15 E-F|15 /	Abcd2	1.27E-08	27.5266

gene_assignment	Gene Symbol	p-value(24h HDM/LPS vs. 24h LPS)	Fold-Change(24h HDM/LPS vs. 24h LPS)
NM_008625 // Mrc1 // mannose receptor, C type 1 // 2 A2|2 10.46 cM // 17533 /// ENSMUST	Mrc1	1.52E-09	19.1231
NM_177909 // Slc9a9 // solute carrier family 9 (sodium/hydrogen exchanger), member 9 //	Slc9a9	1.20E-08	17.6318
NM_147220 // Abca9 // ATP-binding cassette, sub-family A (ABC1), member 9 // 11 E1|11 /	Abca9	1.23E-09	16.8219
NR_030718 // F630028O10Rik // RIKEN cDNA F630028O10 gene // X C3|X // 100038363 /// ENS	F630028O10Rik	3.87E-08	15.8444
NM_011638 // Tfrc // transferrin receptor // 16 B3|16 23.06 cM // 22042 /// ENSMUST0000	Tfrc	2.01E-11	15.5247
XM_006504587 // Nxpe5 // neurexophilin and PC-esterase domain family, member 5 // 5 G2|	Nxpe5	4.60E-07	13.2704
NM_001204252 // Clec10a // C-type lectin domain family 10, member A // 11 B3|11 42.99 c	Clec10a	2.38E-06	13.1808
NM_007642 // Cd28 // CD28 antigen // 1 C1-C3|1 30.52 cM // 12487 /// ENSMUST00000027165	Cd28	7.70E-08	12.6421
NR_046157 // Gm5086 // predicted gene 5086 // 13 D1|13 // 328314	Gm5086	4.70E-07	11.8449
NM_139138 // Emr4 // EGF-like module containing, mucin-like, hormone receptor-like sequ	Emr4	1.26E-06	11.3012
ENSMUST00000103426 // Ighm // immunoglobulin heavy constant mu // --- // --- /// ENSMUS	Ighm	1.36E-09	10.5823
NM_010517 // Igfbp4 // insulin-like growth factor binding protein 4 // 11 D|11 // 16010	Igfbp4	7.13E-09	10.5244
NM_009888 // Cfh // complement component factor h // 1 F|1 61.62 cM // 12628 /// ENSMUS	Cfh	2.91E-10	9.88262
NM_001013370 // Sesn1 // sestrin 1 // 10 B2|10 22.77 cM // 140742 /// NM_001162908 // S	Sesn1	7.23E-08	9.867
NM_001037937 // Deptor // DEP domain containing MTOR-interacting protein // 15 D1|15 21	Deptor	1.96E-07	9.59837
NM_001252530 // Slco2b1 // solute carrier organic anion transporter family, member 2b1	Slco2b1	7.76E-06	9.12333
NM_008611 // Mmp8 // matrix metallopeptidase 8 // 9 A1|9 // 17394 /// ENSMUST0000001876	Mmp8	2.05E-07	8.79564
NM_029861 // Cnrip1 // cannabinoid receptor interacting protein 1 // 11|11 A3.1 // 3806	Cnrip1	1.18E-06	8.5377
---		0.00321704	8.44661
NM_001130412 // Lpin1 // lipin 1 // 12 A1.1|12 7.9 cM // 14245 /// NM_015763 // Lpin1 /	Lpin1	2.39E-06	8.34154
NM_001252506 // St6gal1 // beta galactoside alpha 2,6 sialyltransferase 1 // 16 B1|16 1	St6gal1	9.37E-08	8.26156
NM_001163495 // Arhgap19 // Rho GTPase activating protein 19 // 19|19 D1 // 71085 /// N	Arhgap19	2.29E-06	8.24015
NM_020008 // Clec7a // C-type lectin domain family 7, member a // 6 F3|6 // 56644 /// E	Clec7a	5.11E-11	8.2215
---		8.13E-05	8.21069
NM_001289740 // Mturn // maturin, neural progenitor differentiation regulator homolog (	Mturn	3.86E-08	8.02225
NM_134066 // Akr1c18 // aldo-keto reductase family 1, member C18 // 13 A1|13 // 105349	Akr1c18	2.82E-06	7.74736
NM_001081278 // Tbc1d4 // TBC1 domain family, member 4 // 14 E2.3|14 // 210789 /// XM_0	Tbc1d4	1.15E-07	7.65743
NM_001037937 // Deptor // DEP domain containing MTOR-interacting protein // 15 D1|15 21	Deptor	2.00E-06	7.59874
NM_001039484 // Kcnj10 // potassium inwardly-rectifying channel, subfamily J, member 10	Kcnj10	9.94E-06	7.56097
NM_133670 // Sult1a1 // sulfotransferase family 1A, phenol-preferring, member 1 // 7 F3	Sult1a1	6.07E-08	7.52235
NM_016917 // Slc40a1 // solute carrier family 40 (iron-regulated transporter), member 1	Slc40a1	5.32E-10	7.38236
NM_177715 // Kctd12 // potassium channel tetramerisation domain containing 12 // 14 E2.	Kctd12	3.92E-09	7.02918
---		0.000962486	6.7899
NM_001166493 // Rasgrp3 // RAS, guanyl releasing protein 3 // 17 E2|17 // 240168 /// NM	Rasgrp3	1.41E-08	6.73383
NM_146008 // Tcp11l2 // t-complex 11 (mouse) like 2 // 10 C1|10 // 216198 /// ENSMUST00	Tcp11l2	1.33E-05	6.69417
---		0.00131646	6.67493
NM_025285 // Stmn2 // stathmin-like 2 // 3 A1|3 2.15 cM // 20257 /// ENSMUST00000029002	Stmn2	2.06E-06	6.58946
---		0.000457687	6.3865
NM_007420 // Adrb2 // adrenergic receptor, beta 2 // 18 E1|18 35.1 cM // 11555 /// ENSM	Adrb2	1.25E-05	6.37003
NM_008830 // Abcb4 // ATP-binding cassette, sub-family B (MDR/TAP), member 4 // 5 A1|5	Abcb4	3.09E-11	6.30977
NM_010016 // Cd55 // CD55 antigen // 1 E4|1 56.89 cM // 13136 /// XM_006529117 // Cd55	Cd55	3.86E-06	6.30499
NM_001190297 // Gpr155 // G protein-coupled receptor 155 // 2 C3|2 // 68526 /// NM_0012	Gpr155	6.64E-06	6.19065
ENSMUST00000103607 // Trav13d-4 // T cell receptor alpha variable 13D-4 // --- // ---	Trav13d-4	1.43E-05	5.88149
NM_001252578 // Sulf2 // sulfatase 2 // 2 H3|2 // 72043 /// NM_001252579 // Sulf2 // su	Sulf2	2.91E-08	5.78565
NM_001170694 // Rcbtb2 // regulator of chromosome condensation (RCC1) and BTB (POZ) dom	Rcbtb2	1.88E-07	5.78306
NM_181401 // Tmem64 // transmembrane protein 64 // 4 A2|4 // 100201 /// ENSMUST00000062	Tmem64	6.89E-08	5.7533
NM_001168491 // Pdcd4 // programmed cell death 4 // 19 D2|19 48.73 cM // 18569 /// NM_0	Pdcd4	9.24E-07	5.69773
NM_172903 // Man2a2 // mannosidase 2, alpha 2 // 7 D2|7 // 140481 /// ENSMUST0000009834	Man2a2	4.95E-10	5.67678
NM_001033872 // Smagp // small cell adhesion glycoprotein // 15 F1|15 // 207818 /// NM_	Smagp	3.40E-06	5.66391
NM_001290633 // Reps2 // RALBP1 associated Eps domain containing protein 2 // X F4|X //	Reps2	4.30E-08	5.61896
NM_001276292 // Wwp1 // WW domain containing E3 ubiquitin protein ligase 1 // 4 A3|4 //	Wwp1	5.45E-10	5.56734
NM_001030289 // Mmp27 // matrix metallopeptidase 27 // 9 A1|9 // 234911 /// XM_00650985	Mmp27	4.59E-09	5.52372
NR_028534 // Snord88c // small nucleolar RNA, C/D box 88C // 7|7 // 100217434 /// ENSMU	Snord88c	0.00240412	5.50916
NM_177378 // Rnf150 // ring finger protein 150 // 8 C2|8 // 330812 /// ENSMUST000000785	Rnf150	8.62E-07	5.46237
NM_019521 // Gas6 // growth arrest specific 6 // 8 A1.1|8 6.06 cM // 14456 /// ENSMUST0	Gas6	3.90E-10	5.3999
NM_001159745 // St8sia4 // ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	St8sia4	4.61E-09	5.35003
---		0.00481451	5.34074
---		0.000429354	5.21336
NM_008548 // Man1a // mannosidase 1, alpha // 10 B3|10 // 17155 /// ENSMUST00000003843	Man1a	1.08E-08	5.19652
---		0.00538369	5.19257
---		0.00186282	5.18253
---		0.00392971	5.14156
NM_027872 // Slc46a3 // solute carrier family 46, member 3 // 5 G3|5 // 71706 /// XM_00	Slc46a3	1.98E-07	5.11488
NM_001113386 // Lifr // leukemia inhibitory factor receptor // 15 A1|15 3.46 cM // 1688	Lifr	3.75E-06	5.11004
NM_009194 // Slc12a2 // solute carrier family 12, member 2 // 18 D3|18 32.15 cM // 2049	Slc12a2	3.99E-07	5.07062
NM_026790 // Ifi27 // interferon, alpha-inducible protein 27 // 12 E|12 52.93 cM // 526	Ifi27	1.69E-06	5.0342
AK143703 // Gm19422 // predicted gene, 19422 // 14|14 50.9 cM // 100502869 /// XM_00651	Gm19422	2.06E-05	5.00368
NM_001166391 // F13a1 // coagulation factor XIII, A1 subunit // 13 A3.3|13 // 74145 ///	F13a1	1.69E-07	4.96518
NM_028390 // Anln // anillin, actin binding protein // 9|9 A4 // 68743 /// XM_006510581	Anln	2.36E-05	4.93853
---		0.00353509	4.93149
NM_177353 // Slc9a7 // solute carrier family 9 (sodium/hydrogen exchanger), member 7 //	Slc9a7	3.31E-07	4.91369
NM_027363 // Chp2 // calcineurin-like EF hand protein 2 // 7|7 F3 // 70261 /// ENSMUST0	Chp2	1.93E-05	4.89503
ENSMUST00000139492 // Gm13710 // predicted gene 13710 // 2 D|2 // 672763	Gm13710	3.57E-05	4.86672
NM_001170333 // Clec4a2 // C-type lectin domain family 4, member a2 // 6 F3|6 58.18 cM	Clec4a2	3.42E-06	4.8594
NM_008969 // Ptgs1 // prostaglandin-endoperoxide synthase 1 // 2 B|2 24.19 cM // 19224	Ptgs1	4.18E-08	4.84567
NM_027343 // Cd209g // CD209g antigen // 8 A1.1|8 // 70192 /// ENSMUST00000130372 // Cd	Cd209g	2.30E-06	4.76302
NM_175406 // Atp6v0d2 // ATPase, H+ transporting, lysosomal V0 subunit D2 // 4 A3|4 //	Atp6v0d2	8.79E-09	4.71221
NM_001146031 // Nrcam // neuron-glia-CAM-related cell adhesion molecule // 12 B3|12 20.	Nrcam	6.68E-05	4.7093
ENSMUST00000090986 // Fcrls // Fc receptor-like S, scavenger receptor // 3 F1|3 // 8089	Fcrls	3.38E-08	4.70319
AK132205 // Gm10554 // predicted gene 10554 // 18 A1|18 // 100038541	Gm10554	0.000102191	4.68893
NM_011075 // Abcb1b // ATP-binding cassette, sub-family B (MDR/TAP), member 1B // 5 A1|	Abcb1b	5.61E-05	4.67575
NM_010753 // Mxd4 // Max dimerization protein 4 // 5 B2|5 17.84 cM // 17122 /// ENSMUST	Mxd4	5.44E-05	4.65655
NM_025877 // Slc25a23 // solute carrier family 25 (mitochondrial carrier; phosphate car	Slc25a23	2.54E-07	4.59158
---		0.0012773	4.58457
---		0.00480842	4.57555
NM_010740 // Cd93 // CD93 antigen // 2 G3|2 73.48 cM // 17064 /// ENSMUST00000099269 //	Cd93	2.34E-08	4.57366
NM_009139 // Ccl6 // chemokine (C-C motif) ligand 6 // 11 C|11 50.85 cM // 20305 /// EN	Ccl6	6.19E-08	4.52214
NM_175366 // Mex3b // mex3 homolog B (C. elegans) // 7 D3|7 47.35 cM // 108797 /// ENSM	Mex3b	1.81E-05	4.49269

NM_001081204 // B3glct // beta-3-glucosyltransferase // 5 G3|5 // 381694 /// ENSMUST000	B3glct	1.54E-05	4.47304
NM_007913 // Egr1 // early growth response 1 // 18 C/D|18 18.76 cM // 13653 /// ENSMUST	Egr1	1.36E-05	4.45971
---		0.00388425	4.45467
NM_001113283 // Fam214a // family with sequence similarity 214, member A // 9 D|9 // 23	Fam214a	3.74E-08	4.43545
NM_011173 // Pros1 // protein S (alpha) // 16 C1.3|16 // 19128 /// ENSMUST00000023629 /	Pros1	3.06E-06	4.36093
NM_010444 // Nr4a1 // nuclear receptor subfamily 4, group A, member 1 // 15|15 F // 153	Nr4a1	1.39E-07	4.34979
NM_008043 // Frat1 // frequently rearranged in advanced T cell lymphomas // 19 C3|19 35	Frat1	7.88E-05	4.34905
ENSMUST00000083940 // Gm25683 // predicted gene, 25683 // --- // ---	Gm25683	0.000160423	4.34073
ENSMUST00000104390 // Gm25631 // predicted gene, 25631 // --- // ---	Gm25631	0.00039016	4.33519
NM_024264 // Cyp27a1 // cytochrome P450, family 27, subfamily a, polypeptide 1 // 1 C3|	Cyp27a1	6.87E-07	4.32338
---		0.00429966	4.30894
---		0.00429966	4.30894
ENSMUST00000157983 // Gm24186 // predicted gene, 24186 // --- // ---	Gm24186	0.00438887	4.30532
NM_011994 // Abcd2 // ATP-binding cassette, sub-family D (ALD), member 2 // 15 E-F|15 /	Abcd2	7.40E-06	4.29056
NM_001242423 // Fam105a // family with sequence similarity 105, member A // 15 B1|15 //	Fam105a	1.51E-06	4.2547
AK047378 // Chst10 // carbohydrate sulfotransferase 10 // 1 B|1 // 98388 /// NM_145142	Chst10	1.42E-05	4.24565
---		0.00331374	4.23619
NM_176837 // Arhgap18 // Rho GTPase activating protein 18 // 10 A4|10 // 73910 /// XM_0	Arhgap18	9.86E-08	4.23322
---		0.000590043	4.23298
NM_011311 // S100a4 // S100 calcium binding protein A4 // 3 F1-F2|3 39.27 cM // 20198 /	S100a4	0.000115173	4.21562
---		0.000477863	4.21078
NR_029535 // Mir99a // microRNA 99a // 16|16 // 387229 /// ENSMUST00000083596 // Mir99a	Mir99a	0.000145776	4.19467
---		0.000972229	4.18512
NM_001289458 // Hgf // hepatocyte growth factor // 5 A2-A3|5 7.07 cM // 15234 /// NM_00	Hgf	7.59E-07	4.18453
NM_174857 // Mamdc2 // MAM domain containing 2 // 19 B|19 // 71738 /// XM_006527345 //	Mamdc2	6.48E-07	4.1777
---		0.0040638	4.14685
AK032971 // Gm11974 // predicted gene 11974 // 11 A1|11 // 100041286	Gm11974	0.000918128	4.10122
NM_001184706 // Tfdp2 // transcription factor Dp 2 // 9 E3.3|9 // 211586 /// NM_0011847	Tfdp2	2.44E-05	4.06039
---		0.00134847	4.05465
NM_001127330 // Pparg // peroxisome proliferator activated receptor gamma // 6 E3-F1|6	Pparg	1.62E-08	4.02496
AK136317 // Gm19816 // predicted gene, 19816 // 3 E1|3 29.17 cM // 100503654	Gm19816	0.000292668	4.00666
NM_001101656 // Gm11710 // predicted gene 11710 // 11 E2|11 // 100043123 /// NM_0011016	Gm11710	6.89E-09	3.98269
NM_133977 // Trf // transferrin // 9 F1-F3|9 55.03 cM // 22041 /// ENSMUST00000035158 /	Trf	2.81E-09	3.98004
NM_020332 // Ank // progressive ankylosis // 15 B1|15 10.23 cM // 11732 /// ENSMUST0000	Ank	1.28E-07	3.97919
NM_001198570 // Abi2 // abl-interactor 2 // 1 C2|1 // 329165 /// NM_001198571 // Abi2 /	Abi2	1.01E-05	3.96162
---		0.00252677	3.94724
ENSMUST00000141541 // Gm15503 // predicted gene 15503 // --- // --- /// XM_006508140 //	Gm15503	8.29E-06	3.941
NM_010513 // Igf1r // insulin-like growth factor I receptor // 7 D1|7 37.27 cM // 16001	Igf1r	3.71E-07	3.93858
---		0.00352524	3.93815
---		0.000904224	3.91254
NM_008008 // Fgf7 // fibroblast growth factor 7 // 2|2 F-G // 14178 /// ENSMUST00000064	Fgf7	5.06E-07	3.8733
NM_001002268 // Gpr126 // G protein-coupled receptor 126 // 10 A2|10 // 215798 /// ENSM	Gpr126	0.000284826	3.87278
NM_008354 // Il12rb2 // interleukin 12 receptor, beta 2 // 6 C1|6 30.81 cM // 16162 ///	Il12rb2	0.000164682	3.86428
NM_133815 // Lbr // lamin B receptor // 1 H5|1 84.89 cM // 98386 /// ENSMUST00000005003	Lbr	6.98E-08	3.85951
NM_011943 // Map2k6 // mitogen-activated protein kinase kinase 6 // 11|11 E1 // 26399 /	Map2k6	7.20E-05	3.84675
---		0.000760334	3.84646
NM_019455 // Hpgds // hematopoietic prostaglandin D synthase // 6|6 D-E // 54486 /// EN	Hpgds	3.00E-07	3.83681
ENSMUST00000082387 // mt-Tf // mitochondrially encoded tRNA phenylalanine // --- // ---	mt-Tf	0.00108203	3.83094
NM_001170537 // Mef2c // myocyte enhancer factor 2C // 13 C3|13 43.68 cM // 17260 /// N	Mef2c	1.74E-08	3.82883
NM_009791 // Aspm // asp (abnormal spindle)-like, microcephaly associated (Drosophila)	Aspm	0.000132014	3.82674
---		0.000282359	3.82285
ENSMUST00000181443 // Gm26778 // predicted gene, 26778 // --- // ---	Gm26778	2.55E-05	3.81126
NM_207161 // Dnph1 // 2-deoxynucleoside 5-phosphate N-hydrolase 1 // 17 C|17 // 381101	Dnph1	0.000426527	3.80679
ENSMUST00000082508 // Gm26225 // predicted gene, 26225 // --- // ---	Gm26225	0.000428496	3.80384
NM_175429 // Kctd12b // potassium channel tetramerisation domain containing 12b // X F3	Kctd12b	1.30E-06	3.79919
---		0.00365792	3.79904
---		0.00194338	3.78955
NM_001205336 // Arap3 // ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3 // 1	Arap3	0.000105374	3.78905
---		0.00489795	3.78207
NM_175930 // Rapgef5 // Rap guanine nucleotide exchange factor (GEF) 5 // 12 F2|12 // 2	Rapgef5	5.38E-08	3.77087
NM_011920 // Abcg2 // ATP-binding cassette, sub-family G (WHITE), member 2 // 6 B3|6 27	Abcg2	2.06E-06	3.77027
NM_010118 // Egr2 // early growth response 2 // 10 B5|10 34.96 cM // 13654 /// XM_00651	Egr2	3.01E-05	3.76818
NM_019861 // Ctsf // cathepsin F // 19 A|19 // 56464 /// ENSMUST00000119694 // Ctsf //	Ctsf	1.82E-06	3.75315
NM_001164763 // Rarres1 // retinoic acid receptor responder (tazarotene induced) 1 // 3	Rarres1	4.83E-05	3.75176
NM_175116 // Lpar6 // lysophosphatidic acid receptor 6 // 14 D3|14 // 67168 /// ENSMUST	Lpar6	6.62E-08	3.71997
NM_178912 // Fancm // Fanconi anemia, complementation group M // 12 C1|12 27.21 cM // 1	Fancm	0.00107912	3.71019
NM_001174170 // Serpinb2 // serine (or cysteine) peptidase inhibitor, clade B, member 2	Serpinb2	3.91E-09	3.69084
NM_145137 // Mgl2 // macrophage galactose N-acetyl-galactosamine specific lectin 2 // 1	Mgl2	0.00178192	3.68625
---		0.00437657	3.68518
---		0.000729418	3.68518
XM_006527625 // Gpr34 // G protein-coupled receptor 34 // X|X A1.3 // 23890 /// ENSMUST	Gpr34	0.00013596	3.67062
---		3.79E-06	3.65482
NR_002864 // Peg13 // paternally expressed 13 // 15 D3|15 // 353342	Peg13	9.71E-07	3.65028
---		4.54E-05	3.61864
NM_019992 // Stap1 // signal transducing adaptor family member 1 // 5 E1|5 // 56792 ///	Stap1	9.52E-07	3.61259
NM_007681 // Cenpa // centromere protein A // 5 B1|5 16.76 cM // 12615 /// XM_006503708	Cenpa	2.89E-06	3.61232
---		0.00145287	3.61005
NM_001101656 // Gm11710 // predicted gene 11710 // 11 E2|11 // 100043123 /// NM_0011016	Gm11710	2.09E-08	3.59523
NR_015537 // 9230114K14Rik // RIKEN cDNA 9230114K14 gene // 5 C1|5 // 414108 /// ENSMUS	9230114K14Rik	0.000614704	3.58973
ENSMUST00000082406 // mt-Tk // mitochondrially encoded tRNA lysine // --- // ---	mt-Tk	0.00129923	3.58863
NM_009848 // Entpd1 // ectonucleoside triphosphate diphosphohydrolase 1 // 19 C3|19 34.	Entpd1	1.25E-07	3.58389
ENSMUST00000174884 // Gm20475 // predicted gene 20475 // --- // ---	Gm20475	0.000257835	3.5611
NM_010145 // Ephx1 // epoxide hydrolase 1, microsomal // 1 H4|1 84.48 cM // 13849 /// E	Ephx1	3.65E-06	3.5596
ENSMUST00000092459 // Cd300lh // CD300 antigen like family member H // 11 E2|11 // 3825	Cd300lh	0.000210688	3.54683
NM_001166406 // Kif20a // kinesin family member 20A // 18 B1|18 18.69 cM // 19348 /// N	Kif20a	1.78E-06	3.52846
NR_036450 // Gm14403 // predicted gene 14403 // 2 H4|2 // 433520	Gm14403	0.000126853	3.50974
---		0.00302063	3.49968
NM_001111052 // Dclk1 // doublecortin-like kinase 1 // 3|3 D // 13175 /// NM_001111053	Dclk1	1.19E-06	3.49955
NM_009690 // Cd5l // CD5 antigen-like // 3 F1|3 // 11801 /// ENSMUST00000015998 // Cd5l	Cd5l	1.65E-07	3.4991

NM_008079 // Galc // galactosylceramidase // 12 E|12 49.83 cM // 14420 /// ENSMUST00000	Galc	5.19E-06	3.49331
NM_145512 // Sft2d2 // SFT2 domain containing 2 // 1 H2.3|1 // 108735 /// ENSMUST000000	Sft2d2	1.47E-07	3.49013
NM_133198 // Pygl // liver glycogen phosphorylase // 12 C2|12 29.01 cM // 110095 /// EN	Pygl	3.25E-06	3.4713
NM_008425 // Kcnj2 // potassium inwardly-rectifying channel, subfamily J, member 2 // 1	Kcnj2	0.000180537	3.45992
NM_007988 // Fasn // fatty acid synthase // 11 E2|11 84.56 cM // 14104 /// ENSMUST00000	Fasn	2.65E-08	3.45628
NM_001289895 // Tns1 // tensin 1 // 1 C3|1 38.17 cM // 21961 /// NM_027884 // Tns1 // t	Tns1	2.13E-07	3.45471
NM_001146287 // Cables1 // CDK5 and Abl enzyme substrate 1 // 18|18 A2 // 63955 /// NM_	Cables1	0.000977468	3.45047
NM_001161763 // Fmo5 // flavin containing monooxygenase 5 // 3 F2.2|3 // 14263 /// NM_0	Fmo5	1.40E-05	3.44449
NM_175164 // Arhgap26 // Rho GTPase activating protein 26 // 18 B3|18 // 71302 /// XM_0	Arhgap26	4.65E-06	3.43509
NM_152801 // Arhgef6 // Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 // X A5|X	Arhgef6	4.31E-06	3.42958
---		0.00247493	3.42759
NM_144942 // Csad // cysteine sulfinic acid decarboxylase // 15 F3|15 // 246277 /// XM_	Csad	4.17E-06	3.42343
NM_010680 // Lama3 // laminin, alpha 3 // 18 A|18 6.2 cM // 16774 /// ENSMUST0000009207	Lama3	1.25E-06	3.41929
NM_001080944 // Atp8b4 // ATPase, class I, type 8B, member 4 // 2 F1|2 // 241633 /// XM	Atp8b4	6.84E-07	3.40502
NM_001271599 // Sort1 // sortilin 1 // 3 F3|3 // 20661 /// NM_019972 // Sort1 // sortil	Sort1	5.94E-09	3.38153
NM_023223 // Cdc20 // cell division cycle 20 // 4 D2.1|4 // 107995 /// ENSMUST000000065	Cdc20	7.61E-06	3.38087
NM_001195529 // Gm4980 // predicted gene 4980 // 7 E2|7 // 100503386 /// ENSMUST0000017	Gm4980	0.000143364	3.36945
ENSMUST00000180988 // Gm26912 // predicted gene, 26912 // --- // ---	Gm26912	0.000440622	3.36305
NM_001291910 // Adcy9 // adenylate cyclase 9 // 16 B1|16 2.42 cM // 11515 /// NM_009624	Adcy9	9.07E-05	3.35052
NM_177606 // Plekhh2 // pleckstrin homology domain containing, family H (with MyTH4 dom	Plekhh2	5.14E-05	3.3164
---		2.60E-05	3.31252
NM_028372 // Mblac2 // metallo-beta-lactamase domain containing 2 // 13 C3|13 // 72852	Mblac2	9.78E-07	3.31045
NM_001123367 // Gm3448 // predicted gene 3448 // 17 A2|17 // 100041639 /// NM_001123368	Gm3448	1.62E-05	3.3031
NM_001243762 // Clcn5 // chloride channel 5 // X A1.1|X 3.21 cM // 12728 /// ENSMUST000	Clcn5	2.39E-09	3.30056
ENSMUST00000103960 // Gm22935 // predicted gene, 22935 // --- // ---	Gm22935	0.00113592	3.29965
---		0.000307924	3.29902
---		0.00185898	3.27594
ENSMUST00000163881 // Gm17364 // predicted gene, 17364 // --- // ---	Gm17364	0.000129711	3.27038
NM_201609 // Zfp652 // zinc finger protein 652 // 11 D|11 // 268469 /// ENSMUST00000091	Zfp652	1.86E-06	3.27008
NM_053272 // Dhcr24 // 24-dehydrocholesterol reductase // 4 C7|4 // 74754 /// ENSMUST00	Dhcr24	4.81E-09	3.26981
NM_025835 // Pccb // propionyl Coenzyme A carboxylase, beta polypeptide // 9 E4|9 // 66	Pccb	0.000177531	3.26358
NM_013464 // Ahr // aryl-hydrocarbon receptor // 12 A3|12 15.78 cM // 11622 /// ENSMUST	Ahr	5.07E-05	3.26354
---		0.00138343	3.2613
---		0.000711377	3.2611
NM_013599 // Mmp9 // matrix metallopeptidase 9 // 2 H1-H2|2 85.27 cM // 17395 /// ENSMU	Mmp9	4.99E-06	3.25363
NM_008478 // L1cam // L1 cell adhesion molecule // X A6-B|X 37.43 cM // 16728 /// ENSMU	L1cam	0.00095187	3.24735
NM_021334 // Itgax // integrin alpha X // 7 F3|7 // 16411 /// ENSMUST00000033053 // Itg	Itgax	7.03E-06	3.24195
NM_001289915 // Cd83 // CD83 antigen // 13 A4-5|13 21.6 cM // 12522 /// NM_009856 // Cd	Cd83	3.65E-06	3.23811
NM_011369 // Shcbp1 // Shc SH2-domain binding protein 1 // 8|8 A1.2 // 20419 /// ENSMUS	Shcbp1	0.00117839	3.23184
NM_001033257 // Phactr2 // phosphatase and actin regulator 2 // 10 A2|10 // 215789 ///	Phactr2	4.04E-05	3.21777
NM_010330 // Emb // embigin // 13 D2.3|13 // 13723 /// ENSMUST00000022242 // Emb // emb	Emb	3.79E-08	3.21594
NM_010302 // Gna12 // guanine nucleotide binding protein, alpha 12 // 5 G2|5 79.3 cM //	Gna12	5.31E-08	3.21384
NM_001146200 // Pik3cg // phosphoinositide-3-kinase, catalytic, gamma polypeptide // 12	Pik3cg	6.47E-08	3.21165
NM_024245 // Kif23 // kinesin family member 23 // 9 B|9 // 71819 /// ENSMUST00000034815	Kif23	0.000790652	3.19618
NM_175542 // Rttn // rotatin // 18 E4|18 // 246102 /// ENSMUST00000023828 // Rttn // ro	Rttn	6.17E-06	3.19607
NM_007630 // Ccnb2 // cyclin B2 // 9 D|9 // 12442 /// ENSMUST00000034742 // Ccnb2 // cy	Ccnb2	2.29E-05	3.19456
NM_008509 // Lpl // lipoprotein lipase // 8 B3.3|8 33.88 cM // 16956 /// ENSMUST0000001	Lpl	1.84E-07	3.1926
NM_001081426 // Dip2c // DIP2 disco-interacting protein 2 homolog C (Drosophila) // 13	Dip2c	4.19E-06	3.18692
---		0.000599403	3.18687
NM_022881 // Rgs18 // regulator of G-protein signaling 18 // 1 F|1 62.99 cM // 64214 //	Rgs18	4.31E-05	3.17918
NM_172597 // Txndc16 // thioredoxin domain containing 16 // 14|14 C1 // 70561 /// XM_00	Txndc16	1.70E-06	3.15536
ENSMUST00000086363 // Tmem150b // transmembrane protein 150B // 7 A1|7 // 330460 /// NM	Tmem150b	3.59E-05	3.14939
NM_133738 // Antxr2 // anthrax toxin receptor 2 // 5 E3|5 // 71914 /// ENSMUST000000312	Antxr2	6.78E-07	3.14475
NR_003517 // Pisd-ps1 // phosphatidylserine decarboxylase, pseudogene 1 // 11 A1|11 //	Pisd-ps1	0.000269848	3.14111
NM_010615 // Kif11 // kinesin family member 11 // 19 C2|19 // 16551 /// ENSMUST00000012	Kif11	7.48E-08	3.12206
NM_153820 // Arhgap15 // Rho GTPase activating protein 15 // 2 B|2 // 76117 /// XM_0064	Arhgap15	1.56E-05	3.12072
---		0.0036551	3.11708
NR_040616 // A130077B15Rik // RIKEN cDNA A130077B15 gene // 10 D2|10 // 319272	A130077B15Rik	0.000176079	3.11499
NM_018797 // Plxnc1 // plexin C1 // 10|10 C3 // 54712 /// XM_006513895 // Plxnc1 // ple	Plxnc1	2.63E-07	3.11444
NM_001291818 // Rhbdf1 // rhomboid family 1 (Drosophila) // 11 A4|11 18.83 cM // 13650	Rhbdf1	0.000118844	3.1141
NM_001243049 // Atp6v0a1 // ATPase, H+ transporting, lysosomal V0 subunit A1 // 11 D|11	Atp6v0a1	2.28E-06	3.11134
NM_001290376 // Camk1d // calcium/calmodulin-dependent protein kinase ID // 2 A1|2 // 2	Camk1d	6.60E-07	3.1083
NM_145938 // Rpp40 // ribonuclease P 40 subunit // 13 A3.3|13 // 208366 /// XM_00651663	Rpp40	0.000893567	3.10772
NM_011121 // Plk1 // polo-like kinase 1 // 7 F3|7 65.52 cM // 18817 /// ENSMUST00000033	Plk1	6.45E-06	3.10227
NM_144546 // Zfp119a // zinc finger protein 119a // 17 D|17 // 104349 /// XM_006523384	Zfp119a	0.00303568	3.10008
NM_027526 // Rasgef1a // RasGEF domain family, member 1A // 6 F1|6 // 70727 /// XM_0065	Rasgef1a	0.0003799	3.08939
NM_007929 // Emp2 // epithelial membrane protein 2 // 16 A1|16 5.54 cM // 13731 /// ENS	Emp2	1.24E-05	3.08197
NM_025806 // Plbd1 // phospholipase B domain containing 1 // 6 G1|6 // 66857 /// ENSMUS	Plbd1	1.11E-05	3.07407
---		0.00353496	3.06691
---		5.98E-05	3.06192
NM_001110233 // Ngfrap1 // nerve growth factor receptor (TNFRSF16) associated protein 1	Ngfrap1	4.73E-06	3.06087
NM_011254 // Rbp1 // retinol binding protein 1, cellular // 9 E3.3|9 51.36 cM // 19659	Rbp1	2.23E-05	3.06008
ENSMUST00000179846 // Gm25121 // predicted gene, 25121 // --- // ---	Gm25121	0.00137242	3.0516
NM_177178 // Lmbrd2 // LMBR1 domain containing 2 // 15 A1|15 // 320506 /// XM_006520092	Lmbrd2	1.42E-06	3.04984
---		0.00364311	3.04217
NM_001081176 // Polr3g // polymerase (RNA) III (DNA directed) polypeptide G // 13 C3|13	Polr3g	2.49E-07	3.04169
NM_019410 // Pfn2 // profilin 2 // 3 D|3 28.15 cM // 18645 /// ENSMUST00000066882 // Pf	Pfn2	1.06E-05	3.04053
---		0.00360467	3.03364
NM_001177625 // Ect2 // ect2 oncogene // 3|3 B // 13605 /// NM_001177626 // Ect2 // ect	Ect2	3.28E-05	3.02803
NM_181595 // Ppp1r9a // protein phosphatase 1, regulatory (inhibitor) subunit 9A // 6 A	Ppp1r9a	9.22E-08	3.02656
NM_011436 // Sorl1 // sortilin-related receptor, LDLR class A repeats-containing // 9 B	Sorl1	9.45E-05	3.02385
NM_001199105 // Trp53inp1 // transformation related protein 53 inducible nuclear protei	Trp53inp1	7.13E-06	3.01239
NM_001290989 // Clstn1 // calsyntenin 1 // 4 E1|4 // 65945 /// NM_023051 // Clstn1 // c	Clstn1	1.58E-06	3.01233
NM_172588 // Serinc5 // serine incorporator 5 // 13 C3|13 // 218442 /// ENSMUST00000049	Serinc5	1.54E-05	3.01111
NM_001033606 // Acsl3 // acyl-CoA synthetase long-chain family member 3 // 1 C4|1 40.84	Acsl3	8.48E-05	3.00604
---		9.72E-06	3.0049
NM_021310 // Jmy // junction-mediating and regulatory protein // 13 C3|13 // 57748 ///	Jmy	1.30E-06	2.99742
NM_175136 // Rnf122 // ring finger protein 122 // 8 A3|8 // 68867 /// XM_006509189 // R	Rnf122	0.000107469	2.98662
NM_008131 // Glul // glutamate-ammonia ligase (glutamine synthetase) // 1 G2|1 // 14645	Glul	1.04E-07	2.98477

NM_001102455 // Aplp2 // amyloid beta (A4) precursor-like protein 2 // 9 A2-B|9 16.66 c	Aplp2	4.33E-08	2.97778
NM_177089 // Tacc1 // transforming, acidic coiled-coil containing protein 1 // 8 A2|8 /	Tacc1	3.86E-06	2.96968
NM_001113209 // Nfib // nuclear factor I/B // 4 C4-C6|4 38.4 cM // 18028 /// NM_0011132	Nfib	3.25E-06	2.96767
NM_013835 // Trove2 // TROVE domain family, member 2 // 1 F|1 62.54 cM // 20822 /// ENS	Trove2	2.14E-06	2.96319
NM_027629 // Pgm2l1 // phosphoglucomutase 2-like 1 // 7|7 F1 // 70974 /// XM_006508205	Pgm2l1	5.11E-07	2.96185
NM_023326 // Bmyc // brain expressed myelocytomatosis oncogene // 2 A3|2 // 107771 ///	Bmyc	0.000197233	2.95565
NM_183116 // Slc18b1 // solute carrier family 18, subfamily B, member 1 // 10 A3-A4|10	Slc18b1	0.000877159	2.95467
NM_001043335 // Eml1 // echinoderm microtubule associated protein like 1 // 12 F1|12 59	Eml1	9.34E-05	2.95437
NM_001164207 // Tmem176b // transmembrane protein 176B // 6 B2.3|6 23.75 cM // 65963 //	Tmem176b	5.41E-06	2.95403
NM_177646 // Dgkd // diacylglycerol kinase, delta // 1 D|1 // 227333 /// XM_006529471 /	Dgkd	5.06E-07	2.95318
NM_011712 // Wbp5 // WW domain binding protein 5 // X F1|X // 22381 /// ENSMUST00000048	Wbp5	0.000232029	2.95111
NM_001287530 // Arhgap6 // Rho GTPase activating protein 6 // X F5|X // 11856 /// NM_00	Arhgap6	3.53E-08	2.93867
NM_026662 // Prps2 // phosphoribosyl pyrophosphate synthetase 2 // X F2-F3|X 78.32 cM /	Prps2	1.40E-06	2.93795
XM_006525694 // Stard4 // StAR-related lipid transfer (START) domain containing 4 // 18	Stard4	0.000215375	2.93055
NM_013743 // Pdk4 // pyruvate dehydrogenase kinase, isoenzyme 4 // 6 A1|6 2.06 cM // 27	Pdk4	3.10E-06	2.92862
NM_001112725 // Aldh3a1 // aldehyde dehydrogenase family 3, subfamily A1 // 11 B2|11 37	Aldh3a1	5.96E-05	2.92427
NM_146251 // Pnpla7 // patatin-like phospholipase domain containing 7 // 2 A3|2 // 2412	Pnpla7	2.24E-06	2.91871
NM_146073 // Zdhhc14 // zinc finger, DHHC domain containing 14 // 17 A1|17 // 224454 //	Zdhhc14	4.53E-06	2.91418
NM_009911 // Cxcr4 // chemokine (C-X-C motif) receptor 4 // 1 E4|1 56.43 cM // 12767 //	Cxcr4	3.43E-06	2.90916
NM_029436 // Klhl24 // kelch-like 24 // 16|16 B1 // 75785 /// ENSMUST00000023509 // Klh	Klhl24	5.96E-05	2.90037
NM_177231 // Arrb1 // arrestin, beta 1 // 7 E2|7 54.09 cM // 109689 /// NM_178220 // Ar	Arrb1	1.25E-08	2.89954
NM_001042699 // Syne3 // spectrin repeat containing, nuclear envelope family member 3 /	Syne3	0.00010986	2.89934
NM_145962 // Pank3 // pantothenate kinase 3 // 11 A4|11 // 211347 /// ENSMUST0000001899	Pank3	1.30E-05	2.89544
ENSMUST00000082479 // Gm22245 // predicted gene, 22245 // --- // ---	Gm22245	7.40E-05	2.88205
ENSMUST00000069568 // Gm9982 // predicted gene 9982 // --- // 791357 /// AK078283 // Gm	Gm9982	0.000390598	2.87828
NR_029728 // Mirlet7c-1 // microRNA let7c-1 // 16|16 // 387246 /// ENSMUST00000083623 /	Mirlet7c-1	0.00149921	2.87664
NM_001039511 // Ivns1abp // influenza virus NS1A binding protein // 1 G2|1 // 117198 //	Ivns1abp	1.38E-06	2.86757
NM_080462 // Hnmt // histamine N-methyltransferase // 2 A3|2 // 140483 /// XM_006497671	Hnmt	1.38E-05	2.86606
NM_001033350 // Bank1 // B cell scaffold protein with ankyrin repeats 1 // 3 G3|3 63.04	Bank1	7.46E-05	2.85436
NM_177184 // Vps13c // vacuolar protein sorting 13C (yeast) // 9 C|9 // 320528 /// ENSM	Vps13c	1.11E-06	2.85277
XR_398829 // LOC102641333 // uncharacterized LOC102641333 // --- // 102641333 /// ENSMU	LOC102641333	0.000292499	2.85246
NM_001286544 // Ccpg1 // cell cycle progression 1 // 9 D|9 40.08 cM // 72278 /// ENSMUS	Ccpg1	1.66E-05	2.85227
---		2.91E-05	2.84706
NM_027547 // Prdm5 // PR domain containing 5 // 6 C1|6 // 70779 /// XR_377491 // Prdm5	Prdm5	0.000842388	2.84448
NM_001042613 // Sepp1 // selenoprotein P, plasma, 1 // 15 A1|15 1.84 cM // 20363 /// NM	Sepp1	1.89E-06	2.84028
NM_001289877 // Per3 // period circadian clock 3 // 4 E2|4 // 18628 /// NM_001289878 //	Per3	1.94E-05	2.83324
ENSMUST00000083348 // Gm24455 // predicted gene, 24455 // --- // --- /// AK161656 // Ta	Gm24455	0.00108394	2.8304
NR_045822 // Gm4890 // predicted gene 4890 // 8 C2|8 // 234479 /// NR_045823 // Gm4890	Gm4890	0.00407254	2.82855
NM_177632 // Fam43a // family with sequence similarity 43, member A // 16 B2|16 // 2240	Fam43a	0.000648594	2.82478
NM_027934 // Rnf180 // ring finger protein 180 // 13|13 D1 // 71816 /// ENSMUST00000069	Rnf180	2.15E-06	2.81835
NM_009441 // Ttc3 // tetratricopeptide repeat domain 3 // 16 C3.3-4|16 55.18 cM // 2212	Ttc3	3.19E-06	2.81638
NM_001291190 // Ssh2 // slingshot homolog 2 (Drosophila) // 11 B5|11 // 237860 /// NM_1	Ssh2	4.46E-07	2.80935
NM_011712 // Wbp5 // WW domain binding protein 5 // X F1|X // 22381 /// ENSMUST00000048	Wbp5	4.21E-05	2.80829
ENSMUST00000106578 // Gm11709 // predicted gene 11709 // --- // ---	Gm11709	0.00208524	2.80392
ENSMUST00000170967 // Rb1 // retinoblastoma 1 // 14 D3|14 38.73 cM // 19645	Rb1	0.000816021	2.80168
NM_001159394 // Nfkbiz // nuclear factor of kappa light polypeptide gene enhancer in B	Nfkbiz	0.00480977	2.79892
NM_181585 // Pik3r3 // phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3	Pik3r3	0.00076148	2.7983
NM_001081189 // Uprt // uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	Uprt	9.05E-07	2.78981
NM_001164275 // Prrg1 // proline rich Gla (G-carboxyglutamic acid) 1 // X B|X // 546336	Prrg1	0.00100796	2.7895
NM_009370 // Tgfbr1 // transforming growth factor, beta receptor I // 4 B1|4 26.02 cM /	Tgfbr1	1.04E-06	2.78632
---		0.000126983	2.78447
NM_001128094 // Atp13a3 // ATPase type 13A3 // 16 B2|16 // 224088 /// NM_001128096 // A	Atp13a3	4.05E-07	2.77817
NM_001288627 // Emp1 // epithelial membrane protein 1 // 6 G1|6 66.25 cM // 13730 /// N	Emp1	2.01E-08	2.7757
NM_178415 // Bbs9 // Bardet-Biedl syndrome 9 (human) // 9 A3|9 // 319845 /// NM_181316	Bbs9	1.92E-05	2.76412
---		0.00393597	2.76196
NM_172595 // Arl15 // ADP-ribosylation factor-like 15 // 13 D2.2|13 // 218639 /// XM_00	Arl15	0.000357624	2.75866
---		0.00256716	2.75699
NM_033314 // Slco2a1 // solute carrier organic anion transporter family, member 2a1 //	Slco2a1	0.000175845	2.75599
NM_001081363 // Cenpf // centromere protein F // 1 H6|1 95.03 cM // 108000 /// XM_00649	Cenpf	3.25E-05	2.75547
NM_001008702 // Dab2 // disabled 2, mitogen-responsive phosphoprotein // 15 A|15 2.15 c	Dab2	2.14E-07	2.75435
NM_007379 // Abca2 // ATP-binding cassette, sub-family A (ABC1), member 2 // 2 A2-B|2 1	Abca2	1.41E-07	2.7501
NR_030609 // Mir511 // microRNA 511 // 2|2 // 100124488 /// ENSMUST00000104704 // Mir51	Mir511	0.000685657	2.74831
NM_181415 // Atrnl1 // attractin like 1 // 19 D2|19 // 226255 /// ENSMUST00000077282 //	Atrnl1	0.000282647	2.74788
NM_022331 // Herpud1 // homocysteine-inducible, endoplasmic reticulum stress-inducible,	Herpud1	1.47E-07	2.7463
NM_001099738 // Dnajc28 // DnaJ (Hsp40) homolog, subfamily C, member 28 // 16 C3.3|16 /	Dnajc28	0.0016587	2.74025
NM_028810 // Rnd3 // Rho family GTPase 3 // 2 C1.1|2 // 74194 /// ENSMUST00000017288 //	Rnd3	3.60E-05	2.73503
NM_178646 // Tigd5 // tigger transposable element derived 5 // 15 D3|15 // 105734 /// E	Tigd5	0.000739989	2.73284
NM_008710 // Nnt // nicotinamide nucleotide transhydrogenase // 13 D2|13 67.21 cM // 18	Nnt	4.49E-07	2.73271
NR_015543 // 2810055G20Rik // RIKEN cDNA 2810055G20 gene // 16 C3.1|16 // 77994 /// ENS	2810055G20Rik	0.00151707	2.73029
NM_001001798 // Atp11c // ATPase, class VI, type 11C // X|X A5 // 320940 /// NM_0010378	Atp11c	1.97E-07	2.7276
NM_033602 // Peli2 // pellino 2 // 14 C1|14 24.6 cM // 93834 /// XM_006519740 // Peli2	Peli2	8.27E-05	2.72502
---		0.00241011	2.72451
NM_019670 // Diap3 // diaphanous homolog 3 (Drosophila) // 14|14 D3 // 56419 /// XM_006	Diap3	0.000138173	2.72246
---		0.00113705	2.72121
NM_011055 // Pde3b // phosphodiesterase 3B, cGMP-inhibited // 7 F1|7 59.46 cM // 18576	Pde3b	0.000103277	2.72012
NM_019730 // Nme3 // NME/NM23 nucleoside diphosphate kinase 3 // 17 A3.3|17 // 79059 //	Nme3	7.44E-05	2.72007
NM_175247 // Zfp28 // zinc finger protein 28 // 7 A1|7 // 22690 /// XM_006539742 // Zfp	Zfp28	0.000163624	2.71721
NM_001040072 // Nynrin // NYN domain and retroviral integrase containing // 14 C3|14 //	Nynrin	0.00201582	2.71532
NM_001170855 // Trim36 // tripartite motif-containing 36 // 18 C|18 24.41 cM // 28105 /	Trim36	0.00131369	2.71382
NM_029631 // Abhd14b // abhydrolase domain containing 14b // 9 F1|9 // 76491 /// XM_006	Abhd14b	0.000185814	2.71145
AK050884 // D030029J20Rik // RIKEN cDNA D030029J20 gene // 2|2 // 100502854	D030029J20Rik	0.000103037	2.71126
NM_016974 // Dbp // D site albumin promoter binding protein // 7 B4|7 29.45 cM // 13170	Dbp	0.000200329	2.70708
NM_001001806 // Zfp36l2 // zinc finger protein 36, C3H type-like 2 // 17 E4|17 // 12193	Zfp36l2	4.78E-07	2.70448
NM_198105 // Fam120c // family with sequence similarity 120, member C // X|X F2 // 2073	Fam120c	1.84E-05	2.70328
NM_010121 // Eif2ak3 // eukaryotic translation initiation factor 2 alpha kinase 3 // 6	Eif2ak3	2.33E-05	2.69706
NM_001034891 // Ermard // ER membrane associated RNA degradation // 17 A2|17 // 381062	Ermard	3.23E-06	2.69695
NM_001102471 // Cnnm2 // cyclin M2 // 19 C3|19 38.97 cM // 94219 /// NM_033569 // Cnnm2	Cnnm2	0.000383708	2.6945
NM_001253708 // Mbnl1 // muscleblind-like 1 (Drosophila) // 3 E1|3 // 56758 /// NM_0012	Mbnl1	5.84E-08	2.69341
NM_026674 // Aph1c // anterior pharynx defective 1c homolog (C. elegans) // 9 C|9 // 68	Aph1c	4.44E-06	2.69296

NM_133721 // Itga9 // integrin alpha 9 // 9 F3|9 70.32 cM // 104099 /// ENSMUST00000044	Itga9	7.92E-05	2.68998
---		0.000495118	2.68974
NM_173442 // Gcnt1 // glucosaminyl (N-acetyl) transferase 1, core 2 // 19 B|19 12.75 cM	Gcnt1	4.71E-05	2.68947
NM_177151 // Vps13b // vacuolar protein sorting 13B (yeast) // 15 B3.1|15 // 666173 ///	Vps13b	6.22E-08	2.68877
XM_006541085 // 2410002F23Rik // RIKEN cDNA 2410002F23 gene // 7 B4|7 // 668661 /// ENS	2410002F23Rik	6.63E-07	2.68743
NM_010764 // Man2b1 // mannosidase 2, alpha B1 // 8 C2|8 41.55 cM // 17159 /// XM_00653	Man2b1	3.00E-07	2.68723
NM_007447 // Ang // angiogenin, ribonuclease, RNase A family, 5 // 14 B-C1|14 26.37 cM	Ang	0.000288553	2.6865
NM_172573 // Engase // endo-beta-N-acetylglucosaminidase // 11 E2|11 // 217364 /// ENSM	Engase	0.000259757	2.68546
NM_145853 // Tpcn1 // two pore channel 1 // 5 F|5 // 252972 /// ENSMUST00000046426 // T	Tpcn1	0.00396998	2.6749
ENSMUST00000150912 // Stard9 // START domain containing 9 // 2 E5|2 // 668880 /// ENSMU	Stard9	1.36E-05	2.67437
NM_013470 // Anxa3 // annexin A3 // 5 E3|5 47.29 cM // 11745 /// ENSMUST00000031447 //	Anxa3	1.44E-07	2.66771
NM_026058 // Cers4 // ceramide synthase 4 // 8|8 A1.2 // 67260 /// XM_006508863 // Cers	Cers4	1.18E-05	2.66645
---		0.00103193	2.66558
NM_027973 // Cenpu // centromere protein U // 8|8 B2 // 71876 /// ENSMUST00000034045 //	Cenpu	0.000938815	2.6655
NM_007836 // Gadd45a // growth arrest and DNA-damage-inducible 45 alpha // 6 C1|6 // 13	Gadd45a	4.46E-07	2.66146
NM_001038604 // Clec5a // C-type lectin domain family 5, member a // 6|6 B2 // 23845 //	Clec5a	1.70E-05	2.66051
AK020421 // Hist1h3d // histone cluster 1, H3d // 13 A2-A3|13 // 319149	Hist1h3d	0.00140555	2.65649
NM_010357 // Gsta4 // glutathione S-transferase, alpha 4 // 9 E1|9 // 14860 /// ENSMUST	Gsta4	5.15E-05	2.65518
---		0.00165309	2.65374
NM_020581 // Angptl4 // angiopoietin-like 4 // 17 B1|17 // 57875 /// ENSMUST00000002360	Angptl4	1.52E-06	2.65372
NM_175158 // Utp20 // UTP20, small subunit (SSU) processome component, homolog (yeast)	Utp20	2.51E-06	2.65236
NM_013881 // Ulk2 // unc-51 like kinase 2 // 11 B2|11 // 29869 /// XM_006533508 // Ulk2	Ulk2	7.50E-06	2.64127
NM_001253822 // Irx3 // Iroquois related homeobox 3 // 8 C5|8 44.55 cM // 16373 /// NM_	Irx3	0.000882374	2.64076
NM_001163336 // Atp2a3 // ATPase, Ca++ transporting, ubiquitous // 11 B4|11 // 53313 //	Atp2a3	0.00369041	2.63739
NM_001190320 // Clec4n // C-type lectin domain family 4, member n // 6 F3|6 58.3 cM //	Clec4n	9.64E-07	2.63653
NM_009592 // Abcb7 // ATP-binding cassette, sub-family B (MDR/TAP), member 7 // X C-D|X	Abcb7	1.95E-06	2.63174
ENSMUST00000140646 // Gm15513 // predicted gene 15513 // --- // ---	Gm15513	0.00239284	2.62594
NM_008514 // Lrp6 // low density lipoprotein receptor-related protein 6 // 6 G1|6 65.37	Lrp6	1.18E-07	2.62453
NM_001123367 // Gm3448 // predicted gene 3448 // 17 A2|17 // 100041639 /// NM_001123368	Gm3448	7.64E-05	2.62376
NM_027495 // Tmem144 // transmembrane protein 144 // 3|3 F1 // 70652 /// XM_006502057 /	Tmem144	0.000220331	2.61758
NM_008628 // Msh2 // mutS homolog 2 (E. coli) // 17 E4|17 57.87 cM // 17685 /// ENSMUST	Msh2	0.000610496	2.61742
NM_009533 // Xrcc5 // X-ray repair complementing defective repair in Chinese hamster ce	Xrcc5	0.000890568	2.61738
NM_007679 // Cebpd // CCAAT/enhancer binding protein (C/EBP), delta // 16 A2|16 10.09 c	Cebpd	0.00100017	2.61385
NM_001081128 // Mtr // 5-methyltetrahydrofolate-homocysteine methyltransferase // 13 A1	Mtr	0.00030823	2.61353
NM_015737 // Galnt4 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosa	Galnt4	0.000232515	2.60389
NM_025840 // Bzw2 // basic leucine zipper and W2 domains 2 // 12|12 B2 // 66912 /// XM_	Bzw2	0.000172654	2.59772
NM_001174155 // Rasgrp4 // RAS guanyl releasing protein 4 // 7 B1|7 16.94 cM // 233046	Rasgrp4	0.000797379	2.59563
NM_175331 // Nt5dc3 // 5-nucleotidase domain containing 3 // 10 C1|10 // 103466 /// ENS	Nt5dc3	7.61E-06	2.5952
XM_006508139 // Rgs10 // regulator of G-protein signalling 10 // 7 F3|7 // 67865 /// NM	Rgs10	0.000100556	2.59345
NM_001037987 // Edil3 // EGF-like repeats and discoidin I-like domains 3 // 13 C3|13 //	Edil3	0.000515843	2.59125
NM_001146010 // Fchsd2 // FCH and double SH3 domains 2 // 7 E3|7 // 207278 /// NM_19901	Fchsd2	7.04E-07	2.58852
NM_177586 // Eif5a2 // eukaryotic translation initiation factor 5A2 // 3 A3|3 // 208691	Eif5a2	1.89E-06	2.58564
NM_009657 // Aldoc // aldolase C, fructose-bisphosphate // 11 B5|11 46.74 cM // 11676 /	Aldoc	4.47E-05	2.58403
NM_026785 // Ube2c // ubiquitin-conjugating enzyme E2C // 2 H3|2 85.27 cM // 68612 ///	Ube2c	0.000320567	2.58333
NM_028370 // Pot1b // protection of telomeres 1B // 17 C|17 // 72836 /// XM_006544959 /	Pot1b	0.000451917	2.58115
---		0.000207327	2.57881
---		0.000207327	2.57881
NM_139232 // Fgd4 // FYVE, RhoGEF and PH domain containing 4 // 16 A3|16 // 224014 ///	Fgd4	1.09E-05	2.57735
NM_172260 // Cep68 // centrosomal protein 68 // 11 A3.1|11 12.92 cM // 216543 /// XM_00	Cep68	0.000100636	2.57365
NM_138672 // Stab1 // stabilin 1 // 14 B|14 // 192187 /// ENSMUST00000036618 // Stab1 /	Stab1	5.58E-08	2.57318
NM_207237 // Man1c1 // mannosidase, alpha, class 1C, member 1 // 4 D3|4 // 230815 /// X	Man1c1	2.30E-06	2.57265
NM_001285831 // Far1 // fatty acyl CoA reductase 1 // 7|7 F2 // 67420 /// NM_027379 //	Far1	6.74E-06	2.57231
---		0.000874605	2.56871
NM_008115 // Gfra2 // glial cell line derived neurotrophic factor family receptor alpha	Gfra2	2.74E-05	2.56861
XM_006496909 // BC055324 // cDNA sequence BC055324 // 1 H2.2|1 // 381306 /// XM_0064969	BC055324	0.00411569	2.5686
NM_001033420 // Dock1 // dedicator of cytokinesis 1 // 7 F3|7 // 330662 /// ENSMUST0000	Dock1	4.22E-05	2.56588
NM_010188 // Fcgr3 // Fc receptor, IgG, low affinity III // 1 H3|1 78.8 cM // 14131 ///	Fcgr3	1.32E-05	2.56239
NM_183390 // Klhl6 // kelch-like 6 // 16 A3|16 // 239743 /// ENSMUST00000058839 // Klhl	Klhl6	7.31E-05	2.56061
NM_134054 // Sptssa // serine palmitoyltransferase, small subunit A // 12 C1|12 // 1047	Sptssa	0.000450197	2.56003
NM_001135149 // Slc39a8 // solute carrier family 39 (metal ion transporter), member 8 /	Slc39a8	3.87E-05	2.55978
NM_170758 // Cd300a // CD300A antigen // 11 E2|11 80.54 cM // 217303 /// XM_006533069 /	Cd300a	8.98E-06	2.55721
ENSMUST00000075558 // Hist2h3b // histone cluster 2, H3b // 3 F2.1|3 // 319154 /// ENSM	Hist2h3b	0.00385528	2.55715
NM_145466 // Ggact // gamma-glutamylamine cyclotransferase // 14 E5|14 // 223267 /// XM	Ggact	0.000280921	2.55626
NM_145443 // L2hgdh // L-2-hydroxyglutarate dehydrogenase // 12 C2|12 // 217666 /// ENS	L2hgdh	0.0039648	2.55431
NM_001110780 // Syn1 // synapsin I // X A1-A4|X 16.37 cM // 20964 /// NM_013680 // Syn1	Syn1	6.73E-05	2.55369
ENSMUST00000101077 // A530017D24Rik // RIKEN cDNA A530017D24 gene // --- // --- /// ENS	A530017D24Ril	3.81E-05	2.5535
NM_001085383 // Anxa9 // annexin A9 // 3|3 F2 // 71790 /// NM_023628 // Anxa9 // annexi	Anxa9	6.57E-05	2.55124
NM_133898 // N4bp2l1 // NEDD4 binding protein 2-like 1 // 5 G3|5 // 100637 /// ENSMUST0	N4bp2l1	4.77E-05	2.54656
NM_019656 // Tspan6 // tetraspanin 6 // X E3|X // 56496 /// ENSMUST00000087557 // Tspan	Tspan6	0.000506803	2.54645
ENSMUST00000082387 // mt-Tf // mitochondrially encoded tRNA phenylalanine // --- // ---	mt-Tf	0.00535983	2.54641
NM_207301 // Wrb // tryptophan rich basic protein // 16 C4|16 // 71446 /// XM_006523091	Wrb	9.11E-05	2.54398
NM_001045513 // Raph1 // Ras association (RalGDS/AF-6) and pleckstrin homology domains	Raph1	0.00016159	2.54167
NM_010497 // Idh1 // isocitrate dehydrogenase 1 (NADP+), soluble // 1 C2|1 32.91 cM //	Idh1	2.32E-07	2.54011
NM_001134829 // Lpgat1 // lysophosphatidylglycerol acyltransferase 1 // 1 H6|1 // 22685	Lpgat1	7.85E-06	2.53881
NM_009061 // Rgs2 // regulator of G-protein signaling 2 // 1 F|1 62.56 cM // 19735 ///	Rgs2	1.27E-07	2.53859
---		0.000820083	2.53683
NM_145599 // Tmem184c // transmembrane protein 184C // 8 C1|8 // 234463 /// XM_00653085	Tmem184c	8.17E-07	2.53421
---		8.23E-05	2.53397
---		8.23E-05	2.53397
---		0.00516648	2.53213
NM_001135577 // Smim13 // small integral membrane protein 13 // 13A4|13 // 108934 /// E	Smim13	0.000340115	2.52993
NM_146136 // Slc16a4 // solute carrier family 16 (monocarboxylic acid transporters), me	Slc16a4	0.00103224	2.52952
---		7.60E-05	2.52874
NM_011937 // Gnpda1 // glucosamine-6-phosphate deaminase 1 // 18 B3|18 // 26384 /// ENS	Gnpda1	5.49E-06	2.52581
NM_001081433 // Ankrd44 // ankyrin repeat domain 44 // 1 C1.1|1 // 329154 /// ENSMUST00	Ankrd44	1.44E-06	2.52514
---		0.00253136	2.52389
NM_146234 // Mmgt1 // membrane magnesium transporter 1 // X A5|X // 236792 /// ENSMUST0	Mmgt1	2.44E-05	2.52198
NM_199033 // Tsen2 // tRNA splicing endonuclease 2 homolog (S. cerevisiae) // 6 E3|6 //	Tsen2	0.00364448	2.51822
NM_199221 // Cd300lb // CD300 antigen like family member B // 11 E2|11 // 217304 /// EN	Cd300lb	4.29E-07	2.5154

NM_145519 // Farp2 // FERM, RhoGEF and pleckstrin domain protein 2 // 1 D|1 // 227377 /	Farp2	0.000227654	2.51285
NM_025314 // Dtd1 // D-tyrosyl-tRNA deacylase 1 // 2|2 H1 // 66044 /// ENSMUST000000289	Dtd1	3.34E-06	2.5126
NM_175507 // Slc35g1 // solute carrier family 35, member G1 // 19 C3|19 // 240660 /// E	Slc35g1	6.56E-05	2.50934
NM_008706 // Nqo1 // NAD(P)H dehydrogenase, quinone 1 // 8 D3|8 54.08 cM // 18104 /// E	Nqo1	6.11E-07	2.5078
---		0.00149701	2.50412
NM_008855 // Prkcb // protein kinase C, beta // 7 F3|7 65.75 cM // 18751 /// ENSMUST000	Prkcb	7.25E-07	2.50325
NM_026482 // Atp2b1 // ATPase, Ca++ transporting, plasma membrane 1 // 10|10 C3 // 6797	Atp2b1	5.51E-06	2.50278
NM_026178 // Mmd // monocyte to macrophage differentiation-associated // 11 C|11 // 674	Mmd	6.44E-06	2.50069
NM_030098 // Rnase6 // ribonuclease, RNase A family, 6 // 14 C1|14 // 78416 /// ENSMUST	Rnase6	3.07E-05	2.49901
NM_010511 // Ifngr1 // interferon gamma receptor 1 // 10 A3|10 8.49 cM // 15979 /// ENS	Ifngr1	3.13E-05	2.49792
NM_019654 // Socs5 // suppressor of cytokine signaling 5 // 17 E4|17 // 56468 /// XM_00	Socs5	0.000432248	2.49713
NM_001290805 // Kif3a // kinesin family member 3A // 11 A5-B1|11 31.97 cM // 16568 ///	Kif3a	5.89E-07	2.49303
NM_172619 // Adamts10 // a disintegrin-like and metallopeptidase (reprolysin type) with	Adamts10	0.0005632	2.48898
NM_009828 // Ccna2 // cyclin A2 // 3 B|3 17.67 cM // 12428 /// ENSMUST00000029270 // Cc	Ccna2	4.54E-06	2.48756
XR_376691 // Adam22 // a disintegrin and metallopeptidase domain 22 // 5 A1|5 3.39 cM /	Adam22	0.000579776	2.48279
NM_177325 // Tsr1 // TSR1 20S rRNA accumulation // 11 B5|11 // 104662 /// ENSMUST000000	Tsr1	0.000171877	2.48102
NM_010633 // Uhmk1 // U2AF homology motif (UHM) kinase 1 // 1|1 H2 // 16589 /// ENSMUST	Uhmk1	9.12E-07	2.47988
NM_011507 // Suclg2 // succinate-Coenzyme A ligase, GDP-forming, beta subunit // 6 D3|6	Suclg2	1.22E-06	2.47687
NM_183046 // Kif20b // kinesin family member 20B // 19 C2|19 // 240641 /// ENSMUST00000	Kif20b	1.44E-05	2.47623
AK085917 // 2610209C05Rik // RIKEN cDNA 2610209C05 gene // 6|6 // 70449 /// AK016706 //	2610209C05Rik	0.000120288	2.47515
NM_001115130 // Zbtb44 // zinc finger and BTB domain containing 44 // 9 A4|9 // 235132	Zbtb44	6.14E-06	2.46528
NM_024223 // Crip2 // cysteine rich protein 2 // 12 F1|12 61.57 cM // 68337 /// XM_0065	Crip2	0.000129804	2.46455
NM_001037955 // Dusp22 // dual specificity phosphatase 22 // 13 A3.2|13 // 105352 /// N	Dusp22	3.69E-07	2.46181
NM_001110843 // Cacna2d1 // calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	8.43E-05	2.46168
NM_001160235 // Fam168b // family with sequence similarity 168, member B // 1 B|1 // 21	Fam168b	1.80E-06	2.46052
NM_008624 // Mras // muscle and microspikes RAS // 9 E3.3|9 // 17532 /// XM_006510826 /	Mras	0.000218478	2.45582
NM_001100449 // Taf4b // TAF4B RNA polymerase II, TATA box binding protein (TBP)-associ	Taf4b	0.000167241	2.4526
---		0.00375646	2.45209
---		0.000439411	2.44622
NM_176996 // Smo // smoothened homolog (Drosophila) // 6 A3.3|6 12.36 cM // 319757 ///	Smo	9.73E-05	2.44377
NM_028131 // Cenpn // centromere protein N // 8 E1|8 // 72155 /// ENSMUST00000034205 //	Cenpn	0.00034282	2.44332
NM_001177572 // Slc25a13 // solute carrier family 25 (mitochondrial carrier, adenine nu	Slc25a13	0.00354006	2.43687
NM_001081252 // Uggt2 // UDP-glucose glycoprotein glucosyltransferase 2 // 14 E4|14 //	Uggt2	5.47E-05	2.43667
NM_023284 // Nuf2 // NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Nuf2	0.000311847	2.43625
NM_029249 // Parpbp // PARP1 binding protein // 10 C2|10 // 75317 /// ENSMUST0000004851	Parpbp	0.00116439	2.43617
NM_028335 // Zfp248 // zinc finger protein 248 // 6 F1|6 // 72720 /// XM_006506676 // Z	Zfp248	7.70E-05	2.43335
NM_178653 // Sccpdh // saccharopine dehydrogenase (putative) // 1 H4|1 // 109232 /// EN	Sccpdh	6.30E-05	2.43324
NM_001164362 // Cep55 // centrosomal protein 55 // 19|19 C3 // 74107 /// NM_028293 // C	Cep55	0.00133479	2.43059
NM_010028 // Ddx3x // DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked // X A1.	Ddx3x	0.00056903	2.42982
NM_001163713 // Tufm // Tu translation elongation factor, mitochondrial // 7 F3|7 // 23	Tufm	0.00500303	2.42828
NM_001282000 // Rbl2 // retinoblastoma-like 2 // 8 C5|8 44.25 cM // 19651 /// NM_001282	Rbl2	5.26E-09	2.42616
NM_010137 // Epas1 // endothelial PAS domain protein 1 // 17 E4|17 // 13819 /// ENSMUST	Epas1	6.73E-05	2.42334
NM_029701 // Spcs3 // signal peptidase complex subunit 3 homolog (S. cerevisiae) // 8 B	Spcs3	2.28E-06	2.42303
NM_010189 // Fcgrt // Fc receptor, IgG, alpha chain transporter // 7 B4|7 29.12 cM // 1	Fcgrt	1.08E-05	2.4217
NR_030499 // Mir505 // microRNA 505 // X|X // 751545 /// ENSMUST00000093573 // Mir505 /	Mir505	0.00340978	2.42139
NM_178929 // Kazald1 // Kazal-type serine peptidase inhibitor domain 1 // 19 C3|19 // 1	Kazald1	0.00448664	2.42075
NM_175403 // Mlec // malectin // 5 F|5 55.99 cM // 109154 /// ENSMUST00000053271 // Mle	Mlec	7.00E-08	2.42073
NM_001123367 // Gm3448 // predicted gene 3448 // 17 A2|17 // 100041639 /// NM_001123368	Gm3448	0.000159604	2.42061
---		0.00320475	2.41975
NM_011334 // Clcn4-2 // chloride channel 4-2 // 7 A1|7 4.23 cM // 12727 /// XM_00653950	Clcn4-2	2.17E-05	2.41928
NM_001081680 // Zfp72 // zinc finger protein 72 // 13 C1|13 // 238722 /// ENSMUST000000	Zfp72	0.00517892	2.41865
ENSMUST00000169406 // Gm1818 // predicted gene 1818 // 12 B3|12 // 217536 /// M74555 //	Gm1818	0.000378154	2.41583
NM_008892 // Pola1 // polymerase (DNA directed), alpha 1 // X C-D|X 41.06 cM // 18968 /	Pola1	0.000146094	2.41541
NM_019487 // Hebp2 // heme binding protein 2 // 10|10 A2 // 56016 /// ENSMUST0000002000	Hebp2	0.00202498	2.41456
NM_144860 // Mib1 // mindbomb homolog 1 (Drosophila) // 18 A1|18 // 225164 /// XM_00652	Mib1	3.24E-05	2.41437
NM_031191 // Prl2c2 // prolactin family 2, subfamily c, member 2 // 13 A1|13 5.18 cM //	Prl2c2	0.00385749	2.41384
NM_008568 // Mcm7 // minichromosome maintenance deficient 7 (S. cerevisiae) // 5|5 G1 /	Mcm7	6.14E-07	2.41059
NM_019864 // Atr // ataxia telangiectasia and Rad3 related // 9 E4|9 // 245000 /// ENSM	Atr	0.000249444	2.40929
NM_022018 // Fam129a // family with sequence similarity 129, member A // 1 G2|1 // 6391	Fam129a	2.67E-06	2.40873
NM_007472 // Aqp1 // aquaporin 1 // 6 B3|6 27.38 cM // 11826 /// ENSMUST00000004774 //	Aqp1	0.00538278	2.40764
NM_001291211 // Pcmtd2 // protein-L-isoaspartate (D-aspartate) O-methyltransferase doma	Pcmtd2	1.42E-05	2.40735
---		0.00232149	2.40711
NM_010146 // Epm2a // epilepsy, progressive myoclonic epilepsy, type 2 gene alpha // 10	Epm2a	0.000376338	2.40407
NM_001110337 // Gprc5c // G protein-coupled receptor, family C, group 5, member C // 11	Gprc5c	4.49E-05	2.40239
NM_001252192 // Eya1 // eyes absent 1 homolog (Drosophila) // 1 A3|1 4.31 cM // 14048 /	Eya1	4.82E-06	2.40226
NM_212445 // Kdelc2 // KDEL (Lys-Asp-Glu-Leu) containing 2 // 9 A5.3|9 // 68304 /// ENS	Kdelc2	4.58E-05	2.40103
NM_010831 // Sik1 // salt inducible kinase 1 // 17 B1|17 17.25 cM // 17691 /// ENSMUST0	Sik1	0.00138225	2.39648
NM_010576 // Itga4 // integrin alpha 4 // 2 C3|2 47.38 cM // 16401 /// ENSMUST000000999	Itga4	1.36E-05	2.39574
NM_010864 // Myo5a // myosin VA // 9 D|9 42.26 cM // 17918 /// ENSMUST00000123128 // My	Myo5a	1.01E-07	2.39492
NM_001163640 // Chn2 // chimerin 2 // 6 B3|6 // 69993 /// NM_023543 // Chn2 // chimerin	Chn2	0.000473274	2.39345
---		0.000716631	2.39181
NM_080855 // Zcchc14 // zinc finger, CCHC domain containing 14 // 8 E1|8 // 142682 ///	Zcchc14	0.00119	2.39059
---		0.000539799	2.39012
---		0.00305038	2.38896
NM_001276452 // Slc17a5 // solute carrier family 17 (anion/sugar transporter), member 5	Slc17a5	5.79E-06	2.38623
NM_183308 // Pon2 // paraoxonase 2 // 6 A1|6 1.99 cM // 330260 /// ENSMUST00000057792 /	Pon2	2.21E-05	2.38604
NM_001081392 // Mdn1 // midasin homolog (yeast) // 4 A5|4 14.3 cM // 100019 /// ENSMUST	Mdn1	4.24E-05	2.38587
NM_028233 // Lrpprc // leucine-rich PPR-motif containing // 17 E4|17 // 72416 /// ENSMU	Lrpprc	5.70E-07	2.38353
---		0.00149548	2.38352
NM_010288 // Gja1 // gap junction protein, alpha 1 // 10 B4|10 28.64 cM // 14609 /// EN	Gja1	7.03E-06	2.38287
NM_144916 // Tmem150a // transmembrane protein 150A // 6 C1|6 // 232086 /// ENSMUST0000	Tmem150a	1.29E-05	2.3821
NM_001290993 // Slc30a4 // solute carrier family 30 (zinc transporter), member 4 // 2 E	Slc30a4	1.20E-06	2.38091
NM_009517 // Zmat3 // zinc finger matrin type 3 // 3|3 B // 22401 /// ENSMUST0000002919	Zmat3	0.000122793	2.38086
XR_387077 // Ap1s2 // adaptor-related protein complex 1, sigma 2 subunit // X F5|X // 1	Ap1s2	1.52E-06	2.37968
NM_001136073 // Nfatc2 // nuclear factor of activated T cells, cytoplasmic, calcineurin	Nfatc2	1.12E-05	2.37811
NM_001037859 // Csf1r // colony stimulating factor 1 receptor // 18 D|18 34.41 cM // 12	Csf1r	4.95E-08	2.37746
XM_006527412 // Rab3il1 // RAB3A interacting protein (rabin3)-like 1 // 19 A|19 // 7476	Rab3il1	4.42E-06	2.37706
NM_025557 // Pcp4l1 // Purkinje cell protein 4-like 1 // 1 H3|1 // 66425 /// XM_0064969	Pcp4l1	0.00100998	2.37476
---		0.00446875	2.37434

NM_001289522 // Cad // carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, an	Cad	2.95E-05	2.3724
NM_001290308 // Col12a1 // collagen, type XII, alpha 1 // 9 E1|9 43.82 cM // 12816 ///	Col12a1	0.000172718	2.37177
NM_001159369 // Polq // polymerase (DNA directed), theta // 16 B3|16 26.32 cM // 77782	Polq	0.000114734	2.37099
NM_030724 // Uck2 // uridine-cytidine kinase 2 // 1 H2.3|1 // 80914 /// XM_006497039 //	Uck2	1.52E-05	2.37088
NM_172514 // Tmem71 // transmembrane protein 71 // 15 D2|15 // 213068 /// ENSMUST000000	Tmem71	0.000130557	2.3705
NM_198308 // Pdpr // pyruvate dehydrogenase phosphatase regulatory subunit // 8 E1|8 //	Pdpr	3.95E-05	2.36718
NM_008605 // Mmp12 // matrix metallopeptidase 12 // 9 A1|9 2.46 cM // 17381 /// XM_0065	Mmp12	1.00E-07	2.36714
NM_008885 // Pmp22 // peripheral myelin protein 22 // 11 B3|11 38.99 cM // 18858 /// EN	Pmp22	3.10E-06	2.3656
NM_011576 // Tfpi // tissue factor pathway inhibitor // 2 D|2 // 21788 /// XM_006499148	Tfpi	0.00493388	2.3642
ENSMUST00000153599 // Gm11940 // predicted gene 11940 // --- // ---	Gm11940	0.00239234	2.36399
NM_172600 // Tmem260 // transmembrane protein 260 // 14 C1|14 // 218989 /// XM_00651883	Tmem260	7.09E-05	2.36139
---		3.97E-05	2.35764
NM_001004140 // Ckap2 // cytoskeleton associated protein 2 // 8 A2|8 // 80986 /// XM_00	Ckap2	2.68E-06	2.35704
NM_001271587 // Eps8 // epidermal growth factor receptor pathway substrate 8 // 6 G1|6	Eps8	5.61E-05	2.35652
NM_001164099 // Add3 // adducin 3 (gamma) // 19 D2|19 47.18 cM // 27360 /// NM_00116410	Add3	0.000514158	2.35313
NM_183195 // Marveld1 // MARVEL (membrane-associating) domain containing 1 // 19 C3|19	Marveld1	0.000221593	2.34922
NM_172616 // C330027C09Rik // RIKEN cDNA C330027C09 gene // 16 B5|16 // 224171 /// ENSM	C330027C09Rik	0.00018978	2.34826
NM_172443 // Tbc1d16 // TBC1 domain family, member 16 // 11 E2|11 // 207592 /// ENSMUST	Tbc1d16	0.00026492	2.34629
ENSMUST00000113438 // Adamts9 // a disintegrin-like and metallopeptidase (reprolysin ty	Adamts9	0.00269444	2.34618
NM_001167914 // Atxn3 // ataxin 3 // 12 E|12 // 110616 /// NM_029705 // Atxn3 // ataxin	Atxn3	1.41E-05	2.34485
NM_178711 // Plscr4 // phospholipid scramblase 4 // 9 E3.3|9 // 235527 /// ENSMUST00000	Plscr4	0.000147885	2.34293
NM_013454 // Abca1 // ATP-binding cassette, sub-family A (ABC1), member 1 // 4 A5-B3|4	Abca1	1.32E-09	2.34291
---		0.00329738	2.3414
NM_009072 // Rock2 // Rho-associated coiled-coil containing protein kinase 2 // 12|12 A	Rock2	3.92E-05	2.33984
NM_008823 // Cfp // complement factor properdin // X A3|X 16.44 cM // 18636 /// XR_3868	Cfp	8.33E-06	2.33979
NM_001098222 // Bhlhb9 // basic helix-loop-helix domain containing, class B9 // X F1|X	Bhlhb9	0.00202418	2.33936
NM_011352 // Sema7a // sema domain, immunoglobulin domain (Ig), and GPI membrane anchor	Sema7a	3.59E-06	2.33705
NM_001098271 // Tmem176a // transmembrane protein 176A // 6 B2.3|6 // 66058 /// NM_0253	Tmem176a	0.00128472	2.33558
NM_028493 // Rhobtb3 // Rho-related BTB domain containing 3 // 13 C1|13 // 73296 /// EN	Rhobtb3	0.000708657	2.33508
NM_052976 // Ophn1 // oligophrenin 1 // X|X C2 // 94190 /// ENSMUST00000033560 // Ophn1	Ophn1	1.93E-06	2.33361
NM_010139 // Epha2 // Eph receptor A2 // 4 D-E|4 73.67 cM // 13836 /// ENSMUST000000066	Epha2	0.00123599	2.33247
NM_010424 // Hfe // hemochromatosis // 13 A2-A4|13 9.88 cM // 15216 /// XM_006516556 //	Hfe	3.96E-05	2.3324
---		0.00123766	2.33187
NM_024288 // Rmnd5a // required for meiotic nuclear division 5 homolog A (S. cerevisiae	Rmnd5a	5.91E-05	2.3303
NM_030263 // Psd3 // pleckstrin and Sec7 domain containing 3 // 8 B3.3|8 // 234353 ///	Psd3	0.00108267	2.32752
NR_039562 // Mir5103 // microRNA 5103 // 1|1 13.22 cM // 100628580 /// ENSMUST000001751	Mir5103	1.10E-05	2.32648
ENSMUST00000153830 // Fam213a // family with sequence similarity 213, member A // 14 B|	Fam213a	1.95E-05	2.32555
NM_008292 // Hsd17b4 // hydroxysteroid (17-beta) dehydrogenase 4 // 18 D1|18 // 15488 /	Hsd17b4	3.03E-06	2.32295
---		0.000335894	2.32115
NM_001163616 // 1810011H11Rik // RIKEN cDNA 1810011H11 gene // 14 B|14 // 69069 /// XR_	1810011H11Rik	0.00035441	2.31871
NM_001113470 // Ctdsp2 // CTD (carboxy-terminal domain, RNA polymerase II, polypeptide	Ctdsp2	1.47E-05	2.31511
NM_009769 // Klf5 // Kruppel-like factor 5 // 14 E2.2|14 // 12224 /// ENSMUST0000000527	Klf5	0.000590116	2.31084
NM_001033167 // Slc22a23 // solute carrier family 22, member 23 // 13 A3.3|13 // 73102	Slc22a23	0.000354847	2.31065
NM_001110231 // Celf2 // CUGBP, Elav-like family member 2 // 2|2 A2-A3 // 14007 /// NM_	Celf2	1.28E-05	2.30556
ENSMUST00000083266 // Gm24613 // predicted gene, 24613 // --- // ---	Gm24613	0.00153974	2.30278
NM_008026 // Fli1 // Friend leukemia integration 1 // 9 A4|9 17.74 cM // 14247 /// XM_0	Fli1	1.86E-06	2.30278
NM_172134 // Pdxk // pyridoxal (pyridoxine, vitamin B6) kinase // 10 C1|10 39.72 cM //	Pdxk	2.09E-05	2.30248
NM_001011782 // Olfr543 // olfactory receptor 543 // 7 E3|7 // 257947 /// ENSMUST000000	Olfr543	0.0051367	2.30031
NM_008924 // Prkar2a // protein kinase, cAMP dependent regulatory, type II alpha // 9 F	Prkar2a	4.05E-06	2.29886
NM_026268 // Dusp6 // dual specificity phosphatase 6 // 10|10 C3 // 67603 /// ENSMUST00	Dusp6	2.55E-07	2.29812
NM_007763 // Crip1 // cysteine-rich protein 1 (intestinal) // 12 F1|12 61.59 cM // 1292	Crip1	0.000163911	2.29679
NM_172617 // Zfp523 // zinc finger protein 523 // 17 A3.3|17 // 224656 /// XR_385316 //	Zfp523	2.60E-05	2.29576
NM_198605 // Ska3 // spindle and kinetochore associated complex subunit 3 // 14 C3|14 /	Ska3	0.000121069	2.29406
NM_010421 // Hexa // hexosaminidase A // 9 B|9 32.02 cM // 15211 /// ENSMUST00000026262	Hexa	5.05E-08	2.29395
NM_175514 // Fam171b // family with sequence similarity 171, member B // 2 D|2 // 24152	Fam171b	0.00133391	2.29394
NM_009104 // Rrm2 // ribonucleotide reductase M2 // 12 A1.3|12 8.5 cM // 20135 /// ENSM	Rrm2	8.31E-07	2.29365
NM_009730 // Atrn // attractin // 2 F1|2 63.26 cM // 11990 /// ENSMUST00000028781 // At	Atrn	2.06E-06	2.29269
NM_001014973 // Snx13 // sorting nexin 13 // 12 A3|12 // 217463 /// ENSMUST00000048519	Snx13	1.78E-06	2.29127
NM_001081298 // Lphn2 // latrophilin 2 // 3 H3|3 // 99633 /// XM_006502443 // Lphn2 //	Lphn2	8.68E-06	2.28923
NM_001159538 // Fgd2 // FYVE, RhoGEF and PH domain containing 2 // 17 A3.3|17 15.26 cM	Fgd2	0.00187656	2.2892
NM_001123372 // Gm3435 // predicted gene 3435 // 17 A2|17 // 100041621 /// XM_006523370	Gm3435	1.23E-05	2.28881
NM_178600 // Vkorc1 // vitamin K epoxide reductase complex, subunit 1 // 7 F3|7 69.81 c	Vkorc1	2.18E-05	2.28806
---		0.00518008	2.28779
NM_145401 // Prkag2 // protein kinase, AMP-activated, gamma 2 non-catalytic subunit //	Prkag2	1.45E-05	2.28598
NM_008986 // Ptrf // polymerase I and transcript release factor // 11 D|11 63.95 cM //	Ptrf	0.000724049	2.28393
NM_010820 // Mpdz // multiple PDZ domain protein // 4 C3|4 38.0 cM // 17475 /// ENSMUST	Mpdz	0.000727872	2.28352
NM_001080746 // Gtf2i // general transcription factor II I // 5 G2|5 74.48 cM // 14886	Gtf2i	0.000434897	2.28123
NM_001081141 // Gabbr2 // gamma-aminobutyric acid (GABA) B receptor, 2 // 4 B1|4 // 242	Gabbr2	2.36E-05	2.28091
NM_146041 // Gmds // GDP-mannose 4, 6-dehydratase // 13 A3.2|13 // 218138 /// ENSMUST00	Gmds	4.51E-05	2.28074
NM_001171004 // Prkd3 // protein kinase D3 // 17 E3|17 // 75292 /// NM_029239 // Prkd3	Prkd3	3.24E-06	2.28016
NM_133739 // Tmem123 // transmembrane protein 123 // 9 A1|9 // 71929 /// ENSMUST0000005	Tmem123	1.06E-06	2.27769
NM_026514 // Cdc42ep3 // CDC42 effector protein (Rho GTPase binding) 3 // 17 E3|17 // 2	Cdc42ep3	9.52E-08	2.27709
NM_008306 // Ndst1 // N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 // 18|1	Ndst1	1.24E-05	2.27691
ENSMUST00000083425 // Gm23136 // predicted gene, 23136 // --- // ---	Gm23136	0.00395714	2.27523
ENSMUST00000098868 // 2610203C20Rik // RIKEN cDNA 2610203C20 gene // 9 A5.1|9 // 100042	2610203C20Rik	0.00302265	2.27467
NM_181416 // Arhgap11a // Rho GTPase activating protein 11A // 2 E4|2 // 228482 /// ENS	Arhgap11a	0.000125373	2.27185
NM_133762 // Ncapg2 // non-SMC condensin II complex, subunit G2 // 12 F2|12 // 76044 //	Ncapg2	9.20E-05	2.27074
---		0.001481	2.26984
NM_001253706 // Sept6 // septin 6 // X|X A2 // 56526 /// ENSMUST00000053456 // Sept6 //	Sep-06	0.000487891	2.26898
NM_001081117 // Mki67 // antigen identified by monoclonal antibody Ki 67 // 7|7 F3-F5 /	Mki67	0.00314163	2.26893
NM_024188 // Oxct1 // 3-oxoacid CoA transferase 1 // 15 A1|15 // 67041 /// ENSMUST00000	Oxct1	6.27E-06	2.26863
NM_001163513 // Dlg5 // discs, large homolog 5 (Drosophila) // 14 A3|14 // 71228 /// NM	Dlg5	7.00E-06	2.26789
NM_001205095 // Gm4944 // predicted gene 4944 // 17 A3.3|17 // 240038 /// XM_006524228	Gm4944	0.0012717	2.26771
XM_006500510 // Stard9 // START domain containing 9 // 2 E5|2 // 668880 /// ENSMUST0000	Stard9	0.000155784	2.26637
NM_026162 // Plxdc2 // plexin domain containing 2 // 2 A2-A3|2 // 67448 /// ENSMUST0000	Plxdc2	1.75E-06	2.26486
NM_001110015 // Wdr36 // WD repeat domain 36 // 18 B1|18 // 225348 /// NM_001110016 //	Wdr36	6.45E-06	2.2647
NM_146089 // Haus1 // HAUS augmin-like complex, subunit 1 // 18 E3|18 // 225745 /// XM_	Haus1	0.000148878	2.26294
NM_001039959 // Ahnak // AHNAK nucleoprotein (desmoyokin) // 19 A|19 // 66395 /// NM_00	Ahnak	3.16E-07	2.2623
NM_001252525 // Cpeb1 // cytoplasmic polyadenylation element binding protein 1 // 7 D3|	Cpeb1	0.0029661	2.26143

NM_029556 // Clybl // citrate lyase beta like // 14 E5|14 // 69634 /// XM_006519497 //	Clybl	0.000596884	2.25797
NM_001290784 // Ldlrad3 // low density lipoprotein receptor class A domain containing 3	Ldlrad3	0.000382284	2.25548
NM_007960 // Etv1 // ets variant 1 // 12 A3-B1|12 17.99 cM // 14009 /// XM_006514965 //	Etv1	0.00176412	2.2532
NM_009987 // Cx3cr1 // chemokine (C-X3-C motif) receptor 1 // 9 F4|9 // 13051 /// ENSMU	Cx3cr1	0.000244349	2.25135
NM_001030307 // Dkc1 // dyskeratosis congenita 1, dyskerin // X A7.3|X // 245474 /// EN	Dkc1	0.000222363	2.25043
NM_001081347 // Rhobtb1 // Rho-related BTB domain containing 1 // 10|10 B5.1 // 69288 /	Rhobtb1	0.000333148	2.24762
NM_001159559 // Xrcc6bp1 // XRCC6 binding protein 1 // 10 D3|10 // 68876 /// ENSMUST000	Xrcc6bp1	0.0017026	2.24711
NM_198899 // Uggt1 // UDP-glucose glycoprotein glucosyltransferase 1 // 1 B|1 // 320011	Uggt1	1.37E-06	2.2455
NM_001145824 // Hipk3 // homeodomain interacting protein kinase 3 // 2 E2|2 // 15259 //	Hipk3	7.37E-06	2.24304
NM_199029 // Zfp395 // zinc finger protein 395 // 14 D1|14 // 380912 /// ENSMUST0000006	Zfp395	0.00253512	2.24286
NM_001113413 // Rnf13 // ring finger protein 13 // 3 D|3 // 24017 /// XM_006501457 // R	Rnf13	1.08E-07	2.24123
NM_138745 // Mthfd1 // methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methe	Mthfd1	0.000284431	2.24062
NM_024191 // Arl2bp // ADP-ribosylation factor-like 2 binding protein // 8 C5|8 // 1075	Arl2bp	1.20E-07	2.23864
NM_145398 // Casd1 // CAS1 domain containing 1 // 6 A1|6 1.81 cM // 213819 /// XM_00650	Casd1	8.45E-06	2.23843
NM_152817 // Ttc27 // tetratricopeptide repeat domain 27 // 17 E2|17 // 74196 /// XM_00	Ttc27	0.000553869	2.23724
NM_001001144 // Scap // SREBF chaperone // 9 F2|9 59.91 cM // 235623 /// NM_001103162 /	Scap	3.29E-05	2.23654
ENSMUST00000110991 // Slc12a6 // solute carrier family 12, member 6 // 2 E3|2 // 107723	Slc12a6	1.27E-07	2.23632
---		0.00082875	2.23271
NM_001081201 // Dpy19l4 // dpy-19-like 4 (C. elegans) // 4 A1|4 // 381510 /// ENSMUST00	Dpy19l4	6.78E-06	2.22957
NM_008397 // Itga6 // integrin alpha 6 // 2 C2-C3|2 42.79 cM // 16403 /// NM_001277970	Itga6	2.98E-05	2.22922
NM_028964 // Snx29 // sorting nexin 29 // --- // 74478 /// ENSMUST00000122168 // Snx29	Snx29	0.0031073	2.22776
NM_001008549 // Zfp658 // zinc finger protein 658 // 7 B4|7 // 210104 /// ENSMUST000001	Zfp658	0.00292333	2.22652
NM_029870 // Crebrf // CREB3 regulatory factor // 17|17 B1 // 77128 /// XM_006525117 //	Crebrf	0.000179891	2.22645
NM_017391 // Slc5a3 // solute carrier family 5 (inositol transporters), member 3 // 16	Slc5a3	0.000316375	2.22617
NM_177305 // Arl4c // ADP-ribosylation factor-like 4C // 1 D|1 // 320982 /// ENSMUST000	Arl4c	1.43E-05	2.22192
NM_020010 // Cyp51 // cytochrome P450, family 51 // 5 A2|5 2.3 cM // 13121 /// ENSMUST0	Cyp51	1.69E-06	2.21677
---		0.00115168	2.21666
NM_028428 // Fut11 // fucosyltransferase 11 // 14|14 B // 73068 /// ENSMUST00000048016	Fut11	2.88E-06	2.21105
NM_001281929 // Gria3 // glutamate receptor, ionotropic, AMPA3 (alpha 3) // X A3.3-A4|X	Gria3	0.000158145	2.21082
NM_008960 // Pten // phosphatase and tensin homolog // 19 C1|19 28.14 cM // 19211 /// X	Pten	4.23E-08	2.21042
BC031701 // Cxx1c // CAAX box 1C // X A5|X // 72865 /// NM_028375 // Cxx1c // CAAX box	Cxx1c	0.00126655	2.21037
NM_007530 // Bcap29 // B cell receptor associated protein 29 // 12 A3|12 13.63 cM // 12	Bcap29	1.96E-05	2.21036
ENSMUST00000082411 // ND3 // NADH dehydrogenase subunit 3 // --- // 17718 /// AK139029	ND3	0.000161048	2.20978
NM_011234 // Rad51 // RAD51 homolog // 2 F1|2 59.92 cM // 19361 /// ENSMUST00000028795	Rad51	0.00494167	2.20863
NM_018822 // Sgsh // N-sulfoglucosamine sulfohydrolase (sulfamidase) // 11 E2|11 83.36	Sgsh	9.05E-06	2.20801
NM_153526 // Insig1 // insulin induced gene 1 // 5 B1|5 // 231070 /// ENSMUST0000005915	Insig1	3.52E-08	2.20787
NM_001170395 // Cd163 // CD163 antigen // 6 F2|6 // 93671 /// NM_053094 // Cd163 // CD1	Cd163	6.01E-06	2.20589
NM_001199321 // Zfp94 // zinc finger protein 94 // 7 A3|7 10.27 cM // 22756 /// NM_0095	Zfp94	0.000976954	2.20516
---		0.00297532	2.20284
NM_001025570 // Prrx1 // paired related homeobox 1 // 1 H2.1|1 70.53 cM // 18933 /// NM	Prrx1	4.69E-06	2.20218
NM_023603 // Sfpq // splicing factor proline/glutamine rich (polypyrimidine tract bindi	Sfpq	0.000104823	2.20127
---		0.000325586	2.20055
NM_001033145 // 1190002N15Rik // RIKEN cDNA 1190002N15 gene // 9 E3.3|9 // 68861 /// EN	1190002N15Rik	6.65E-05	2.20051
NM_010124 // Eif4ebp2 // eukaryotic translation initiation factor 4E binding protein 2	Eif4ebp2	0.000251589	2.20011
NM_153126 // Nat10 // N-acetyltransferase 10 // 2 E2|2 // 98956 /// XM_006500455 // Nat	Nat10	7.42E-05	2.19992
NR_028478 // Snora75 // small nucleolar RNA, H/ACA box 75 // 1|1 // 100303740 /// ENSMU	Snora75	0.00517368	2.19983
NM_001290662 // Kif2c // kinesin family member 2C // 4 D1|4 53.42 cM // 73804 /// NM_13	Kif2c	0.000108674	2.1993
NM_026598 // Ebpl // emopamil binding protein-like // 14 D1|14 // 68177 /// ENSMUST0000	Ebpl	0.000135718	2.19863
---		0.00266185	2.19848
ENSMUST00000082700 // Gm22620 // predicted gene, 22620 // --- // --- /// AK161656 // Ta	Gm22620	0.00285274	2.19837
NM_001081371 // Dmxl1 // Dmx-like 1 // 18 D1|18 // 240283 /// XM_006525916 // Dmxl1 //	Dmxl1	3.31E-08	2.1981
---		0.0025695	2.19763
NM_026880 // Pink1 // PTEN induced putative kinase 1 // 4 D3|4 // 68943 /// ENSMUST0000	Pink1	7.04E-06	2.19534
NM_009773 // Bub1b // budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevis	Bub1b	0.00179251	2.1953
NM_008152 // Gpr65 // G-protein coupled receptor 65 // 12 E|12 // 14744 /// ENSMUST0000	Gpr65	7.50E-07	2.19529
ENSMUST00000000199 // Ncs1 // neuronal calcium sensor 1 // 2 B|2 // 14299 /// NM_019681	Ncs1	0.00417266	2.19495
---		4.19E-05	2.19375
ENSMUST00000170447 // Rpl28-ps4 // ribosomal protein L28, pseudogene 4 // --- // ---	Rpl28-ps4	0.00516546	2.19341
NM_001081286 // Fat1 // FAT tumor suppressor homolog 1 (Drosophila) // 8 B1.1|8 24.81 c	Fat1	5.93E-05	2.193
NM_011156 // Prep // prolyl endopeptidase // 10 B2-B3|10 23.27 cM // 19072 /// ENSMUST0	Prep	1.97E-05	2.19081
NM_172301 // Ccnb1 // cyclin B1 // 13 D1|13 53.23 cM // 268697 /// ENSMUST00000072119 /	Ccnb1	0.00268129	2.18933
---		0.000811041	2.18805
NM_001285991 // Tbc1d5 // TBC1 domain family, member 5 // 17 C|17 // 72238 /// NM_00128	Tbc1d5	2.86E-05	2.18792
NM_001033219 // Slc45a4 // solute carrier family 45, member 4 // 15 D3|15 // 106068 ///	Slc45a4	0.000761645	2.18587
NM_028015 // Cers5 // ceramide synthase 5 // 15 F1|15 // 71949 /// ENSMUST00000023762 /	Cers5	1.25E-05	2.18328
---		0.000401354	2.18292
NM_001015039 // Zfyve28 // zinc finger, FYVE domain containing 28 // 5 B2|5 // 231125 /	Zfyve28	0.000400408	2.18205
NM_001110265 // Ttk // Ttk protein kinase // 9 E2|9 // 22137 /// NM_001284272 // Ttk //	Ttk	0.000174356	2.18079
---		0.000247632	2.18048
---		0.000282871	2.17785
NM_001122989 // Cdc14b // CDC14 cell division cycle 14B // 13 B3|13 // 218294 /// NM_17	Cdc14b	0.000186532	2.17624
NM_029965 // Rnf170 // ring finger protein 170 // 8|8 // 77733 /// ENSMUST00000014022 /	Rnf170	0.000737883	2.176
---		0.00312149	2.17423
NM_027534 // Kdsr // 3-ketodihydrosphingosine reductase // 1 E2.1|1 // 70750 /// XM_006	Kdsr	0.000302972	2.17198
NM_001199948 // Dynlt1f // dynein light chain Tctex-type 1F // 17 A1|17 // 100040531	Dynlt1f	2.34E-05	2.17097
NM_023057 // Zak // sterile alpha motif and leucine zipper containing kinase AZK // 2 C	Zak	9.01E-05	2.16974
---		0.00376839	2.16898
XM_006515014 // Prkar2b // protein kinase, cAMP dependent regulatory, type II beta // 1	Prkar2b	2.15E-05	2.16892
---		4.58E-06	2.1684
NM_001170643 // Rnf144b // ring finger protein 144B // 13 A5|13 // 218215 /// NM_146042	Rnf144b	0.00012184	2.16832
NM_001081323 // Mphosph9 // M-phase phosphoprotein 9 // 5 F|5 // 269702 /// NM_00127786	Mphosph9	0.000101386	2.16744
NM_001081081 // Gls // glutaminase // 1 C1.1|1 26.86 cM // 14660 /// NM_001113383 // Gl	Gls	1.09E-05	2.1665
NM_025780 // Thap2 // THAP domain containing, apoptosis associated protein 2 // 10 D2|1	Thap2	0.00464203	2.16592
ENSMUST00000104252 // Gm23130 // predicted gene, 23130 // --- // ---	Gm23130	0.000474403	2.16508
NM_001164733 // Mpp6 // membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6	Mpp6	3.61E-05	2.16492
NM_001167885 // Suv420h1 // suppressor of variegation 4-20 homolog 1 (Drosophila) // 19	Suv420h1	1.08E-05	2.16469
NM_001271407 // Sorbs3 // sorbin and SH3 domain containing 3 // 14 D2|14 36.27 cM // 20	Sorbs3	0.000542185	2.16458
NM_001008502 // Bbs12 // Bardet-Biedl syndrome 12 (human) // 3 B|3 // 241950 /// NM_001	Bbs12	0.00374185	2.16138
XM_006510240 // Gramd1b // GRAM domain containing 1B // 9|9 B // 235283 /// NM_172768 /	Gramd1b	6.20E-06	2.15975

NM_011273 // Xpr1 // xenotropic and polytropic retrovirus receptor 1 // 1 G3|1 66.49 cM	Xpr1	6.82E-07	2.15883
NM_144915 // Daglb // diacylglycerol lipase, beta // 5 G2|5 // 231871 /// XM_006504699	Daglb	1.67E-06	2.15831
---		0.000390739	2.15687
NM_012056 // Fkbp9 // FK506 binding protein 9 // 6 B3|6 27.74 cM // 27055 /// ENSMUST00	Fkbp9	1.54E-05	2.15616
---		0.000260041	2.15345
NM_025969 // Timm21 // tranlocase of inner mitochondrial membrane 21 // 18|18 E3 // 671	Timm21	0.0022304	2.15309
NM_025277 // Gng10 // guanine nucleotide binding protein (G protein), gamma 10 // 4 B3|	Gng10	1.13E-05	2.15284
NM_022315 // Smoc2 // SPARC related modular calcium binding 2 // 17 A2|17 8.95 cM // 64	Smoc2	0.00448854	2.15175
NM_010008 // Cyp2j6 // cytochrome P450, family 2, subfamily j, polypeptide 6 // 4 C5|4	Cyp2j6	0.00139978	2.15049
NR_045098 // Gm2115 // predicted gene 2115 // 7 D3|7 // 100039239 /// ENSMUST0000018038	Gm2115	0.00287242	2.14913
NM_010111 // Efnb2 // ephrin B2 // 8 A1.1|8 3.42 cM // 13642 /// ENSMUST00000001319 //	Efnb2	0.00315312	2.14815
NM_001162375 // Fam73a // family with sequence similarity 73, member A // 3 H3|3 // 215	Fam73a	0.000861726	2.14593
NM_028149 // Fbxl20 // F-box and leucine-rich repeat protein 20 // 11 D|11 // 72194 ///	Fbxl20	5.55E-05	2.14228
NM_013589 // Ltbp2 // latent transforming growth factor beta binding protein 2 // 12|12	Ltbp2	0.000139572	2.14213
NM_175518 // Tmem245 // transmembrane protein 245 // 4 B3|4 // 242474 /// ENSMUST000000	Tmem245	7.48E-05	2.14151
NM_001033458 // Gm1673 // predicted gene 1673 // 5 B2|5 // 381633 /// ENSMUST0000009486	Gm1673	0.000353308	2.14124
NM_001146707 // Nap1l1 // nucleosome assembly protein 1-like 1 // 10 D1|10 58.67 cM //	Nap1l1	1.69E-06	2.14026
NM_172882 // Wdfy3 // WD repeat and FYVE domain containing 3 // 5 E4-E5|5 48.95 cM // 7	Wdfy3	1.14E-06	2.13995
NM_133818 // AI597479 // expressed sequence AI597479 // 1 B|1 // 98404 /// ENSMUST00000	AI597479	0.00269686	2.13982
---		0.000531482	2.13955
NM_181547 // Nostrin // nitric oxide synthase trafficker // 2 C2|2 // 329416 /// ENSMUS	Nostrin	6.22E-06	2.13918
---		0.000129176	2.13807
NM_001163687 // Naaa // N-acylethanolamine acid amidase // 5|5 E3 // 67111 /// NM_02597	Naaa	1.06E-06	2.13799
NM_007496 // Zfhx3 // zinc finger homeobox 3 // 8|8 E1 // 11906 /// XM_006530586 // Zfh	Zfhx3	0.000176886	2.13767
NM_175445 // Rassf2 // Ras association (RalGDS/AF-6) domain family member 2 // 2 F2|2 /	Rassf2	3.08E-06	2.13656
NR_028401 // Taf1d // TATA box binding protein (Tbp)-associated factor, RNA polymerase	Taf1d	0.000170675	2.136
---		0.000458928	2.13383
---		0.00451048	2.1338
NM_027903 // Dhdh // dihydrodiol dehydrogenase (dimeric) // 7 B2|7 29.32 cM // 71755 //	Dhdh	4.93E-07	2.13358
NM_001159536 // Adcy3 // adenylate cyclase 3 // 12|12 A-B // 104111 /// NM_001159537 //	Adcy3	0.00199641	2.1331
NR_015597 // Zfp862-ps // zinc finger protein 862, pseudogene // 6 B2.3|6 // 58894 ///	Zfp862-ps	0.00265644	2.13194
NM_028319 // Zfp518a // zinc finger protein 518A // 19 D1|19 // 72672 /// ENSMUST000000	Zfp518a	5.25E-05	2.13129
NM_001159516 // Qk // quaking // 17 A1|17 7.75 cM // 19317 /// NM_001159517 // Qk // qu	Qk	3.37E-06	2.13032
NM_172437 // Pus7l // pseudouridylate synthase 7 homolog (S. cerevisiae)-like // 15 E3|	Pus7l	0.000105359	2.13016
NM_028102 // Ddhd2 // DDHD domain containing 2 // 8|8 A3 // 72108 /// XR_378791 // Ddhd	Ddhd2	5.34E-05	2.12891
ENSMUST00000129570 // Gm11974 // predicted gene 11974 // --- // --- /// AK160548 // Gm1	Gm11974	0.000714235	2.12665
NR_029382 // Mir17hg // Mir17 host gene 1 (non-protein coding) // 14|14 // 75957 /// NR	Mir17hg	0.000866475	2.12661
NM_009128 // Scd2 // stearoyl-Coenzyme A desaturase 2 // 19 C3|19 37.98 cM // 20250 ///	Scd2	3.14E-08	2.12654
NM_011159 // Prkdc // protein kinase, DNA activated, catalytic polypeptide // 16 10.09	Prkdc	0.000110209	2.12582
---		0.00455781	2.12567
---		0.00216441	2.12357
NM_029999 // Lbh // limb-bud and heart // 17 E2|17 // 77889 /// ENSMUST00000024857 // L	Lbh	1.20E-05	2.12312
NM_146019 // Chd3 // chromodomain helicase DNA binding protein 3 // 11 B3|11 // 216848	Chd3	0.0042899	2.11994
NM_028906 // Dpp8 // dipeptidylpeptidase 8 // 9|9 D // 74388 /// XM_006511517 // Dpp8 /	Dpp8	1.53E-06	2.11931
NM_025382 // Tmem57 // transmembrane protein 57 // 4 D3|4 67.11 cM // 66146 /// ENSMUST	Tmem57	2.04E-05	2.11894
NM_001001985 // Nat8l // N-acetyltransferase 8-like // 5 B2|5 // 269642 /// ENSMUST0000	Nat8l	0.0013404	2.11662
NM_011467 // Spr // sepiapterin reductase // 6 C3|6 37.15 cM // 20751 /// ENSMUST000000	Spr	0.0039973	2.11591
NM_012012 // Exo1 // exonuclease 1 // 1 H4|1 81.9 cM // 26909 /// XM_006496862 // Exo1	Exo1	0.000757033	2.11558
NM_001267622 // Ttc28 // tetratricopeptide repeat domain 28 // 5 F|5 // 209683 /// ENSM	Ttc28	0.000556522	2.11512
NM_001290514 // Mospd1 // motile sperm domain containing 1 // X|X A4 // 70380 /// NM_02	Mospd1	7.97E-07	2.11453
NM_007564 // Zfp36l1 // zinc finger protein 36, C3H type-like 1 // 12 C3|12 // 12192 //	Zfp36l1	7.41E-05	2.11272
---		5.74E-05	2.11238
NM_148945 // Rps6ka3 // ribosomal protein S6 kinase polypeptide 3 // X F4|X 73.27 cM //	Rps6ka3	8.20E-06	2.11078
NM_016681 // Chek2 // checkpoint kinase 2 // 5 F|5 // 50883 /// XM_006535068 // Chek2 /	Chek2	0.000178994	2.11004
NM_001285997 // Prc1 // protein regulator of cytokinesis 1 // 7 D3|7 45.62 cM // 233406	Prc1	0.000235381	2.10943
NM_182997 // Prkab2 // protein kinase, AMP-activated, beta 2 non-catalytic subunit // 3	Prkab2	0.000461987	2.10769
NM_001162904 // Mdm1 // transformed mouse 3T3 cell double minute 1 // 10 C1-C3|10 66.65	Mdm1	0.000499884	2.10714
NM_030133 // Srbd1 // S1 RNA binding domain 1 // 17 E4|17 // 78586 /// ENSMUST000000951	Srbd1	0.00508915	2.10677
NM_146126 // Sord // sorbitol dehydrogenase // 2 E5|2 60.59 cM // 20322 /// ENSMUST0000	Sord	4.12E-06	2.10555
NM_175563 // Prr11 // proline rich 11 // 11 C|11 // 270906 /// ENSMUST00000051395 // Pr	Prr11	0.00219805	2.10492
NM_173444 // Nbeal1 // neurobeachin like 1 // 1 C2|1 // 269198 /// XM_006496031 // Nbea	Nbeal1	0.000114463	2.10406
ENSMUST00000180411 // Gm17491 // predicted gene, 17491 // 8|8 11.42 cM // 100502938	Gm17491	5.97E-05	2.10345
NM_001005510 // Syne2 // spectrin repeat containing, nuclear envelope 2 // 12 C3|12 33.	Syne2	0.000796387	2.10281
NM_207541 // Zfp81 // zinc finger protein 81 // 17 B1|17 // 224694 /// ENSMUST000000540	Zfp81	0.00523404	2.10174
NM_001177751 // Tsc22d1 // TSC22 domain family, member 1 // 14 D3|14 40.44 cM // 21807	Tsc22d1	5.13E-06	2.10073
NM_001193271 // Meis1 // Meis homeobox 1 // 11 A3.1|11 11.11 cM // 17268 /// NM_010789	Meis1	0.00132608	2.10071
---		0.00276662	2.10013
NM_019413 // Robo1 // roundabout homolog 1 (Drosophila) // 16 C3.1|16 // 19876 /// XM_0	Robo1	0.000411718	2.09966
NM_021510 // Hnrnph1 // heterogeneous nuclear ribonucleoprotein H1 // 11|11 B1.2 // 590	Hnrnph1	6.86E-05	2.09866
NM_001164046 // Gm13306 // predicted gene 13306 // 4 A5|4 // 100039863 /// NM_001199959	Gm13306	0.00208759	2.09688
NM_001111324 // Nedd9 // neural precursor cell expressed, developmentally down-regulate	Nedd9	0.00014849	2.09655
NM_001081960 // Clasp2 // CLIP associating protein 2 // 9|9 F2 // 76499 /// NM_00111434	Clasp2	7.16E-06	2.09644
NM_001271413 // Nfam1 // Nfat activating molecule with ITAM motif 1 // 15|15 E2 // 7403	Nfam1	8.33E-05	2.09175
NM_134012 // Mbtd1 // mbt domain containing 1 // 11 D|11 // 103537 /// XM_006531889 //	Mbtd1	0.000264142	2.08955
NM_009530 // Atrx // alpha thalassemia/mental retardation syndrome X-linked homolog (hu	Atrx	1.28E-05	2.08929
NM_144908 // Galnt11 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactos	Galnt11	7.74E-05	2.08889
NM_030732 // Tbl1xr1 // transducin (beta)-like 1X-linked receptor 1 // 3 A3|3 // 81004	Tbl1xr1	0.00018273	2.08761
NM_029617 // Casc5 // cancer susceptibility candidate 5 // 2 E5|2 // 76464 /// ENSMUST0	Casc5	0.00299821	2.08624
NM_011086 // Pikfyve // phosphoinositide kinase, FYVE finger containing // 1 C2|1 // 18	Pikfyve	3.69E-06	2.08579
NM_025626 // Fam107b // family with sequence similarity 107, member B // 2 A1|2 // 6654	Fam107b	0.00018985	2.08375
NM_134042 // Aldh6a1 // aldehyde dehydrogenase family 6, subfamily A1 // 12 D1|12 39.21	Aldh6a1	8.18E-05	2.08343
NM_020270 // Scamp5 // secretory carrier membrane protein 5 // 9 B|9 // 56807 /// XM_00	Scamp5	0.000699976	2.08239
NM_011101 // Prkca // protein kinase C, alpha // 11 E1|11 70.8 cM // 18750 /// ENSMUST0	Prkca	6.62E-07	2.08135
NM_025377 // Ska2 // spindle and kinetochore associated complex subunit 2 // 11 C|11 //	Ska2	0.00114395	2.08095
NM_011699 // Lin7c // lin-7 homolog C (C. elegans) // 2 E3|2 56.65 cM // 22343 /// ENSM	Lin7c	1.51E-05	2.08081
NM_027144 // Arhgef12 // Rho guanine nucleotide exchange factor (GEF) 12 // 9|9 B // 69	Arhgef12	1.45E-05	2.0804
NM_026579 // D10Wsu102e // DNA segment, Chr 10, Wayne State University 102, expressed /	D10Wsu102e	0.000218028	2.07971
NM_172779 // Ddx26b // DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B // X A5|X // 23	Ddx26b	0.0013386	2.07885
NM_009142 // Cx3cl1 // chemokine (C-X3-C motif) ligand 1 // 8 C5|8 46.79 cM // 20312 //	Cx3cl1	0.00530959	2.07866

NM_011391 // Slc16a7 // solute carrier family 16 (monocarboxylic acid transporters), me	Slc16a7	3.54E-06	2.07797
---		0.00318876	2.07791
NM_175751 // Zfp608 // zinc finger protein 608 // 18 D3|18 // 269023 /// ENSMUST0000006	Zfp608	0.00517537	2.07675
NM_145437 // Cd300ld // CD300 molecule-like family member d // 11 E2|11 // 217305 /// E	Cd300ld	5.60E-05	2.0767
NM_007691 // Chek1 // checkpoint kinase 1 // 9|9 A5.3 // 12649 /// ENSMUST00000034625 /	Chek1	0.00289499	2.07619
NM_001252494 // Rapgef6 // Rap guanine nucleotide exchange factor (GEF) 6 // 11 B1.3|11	Rapgef6	0.000200745	2.07606
NM_009128 // Scd2 // stearoyl-Coenzyme A desaturase 2 // 19 C3|19 37.98 cM // 20250 ///	Scd2	0.000176755	2.07591
NM_028749 // Npl // N-acetylneuraminate pyruvate lyase // 1|1 G2 // 74091 /// ENSMUST00	Npl	0.0006051	2.07486
NM_053122 // Immp2l // IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	Immp2l	0.00300827	2.07454
NM_001162416 // Pfkfb2 // 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 // 1 E4	Pfkfb2	0.000178318	2.07422
NM_172307 // Mbtps2 // membrane-bound transcription factor peptidase, site 2 // X F4|X	Mbtps2	6.53E-05	2.07258
NM_001042421 // Kntc1 // kinetochore associated 1 // 5 F|5 // 208628 /// XM_006530250 /	Kntc1	0.000446337	2.07247
NM_172467 // Zc3hav1l // zinc finger CCCH-type, antiviral 1-like // 6 B1|6 // 209032 //	Zc3hav1l	0.00194388	2.07066
---		0.000986138	2.0699
NM_013552 // Hmmr // hyaluronan mediated motility receptor (RHAMM) // 11 A5|11 24.4 cM	Hmmr	0.00025175	2.06967
ENSMUST00000046303 // Crebl2 // cAMP responsive element binding protein-like 2 // 6 G1|	Crebl2	0.00211861	2.06864
NM_027906 // Vwa8 // von Willebrand factor A domain containing 8 // 14 D3|14 // 219189	Vwa8	1.15E-05	2.06812
NM_177660 // Zbtb10 // zinc finger and BTB domain containing 10 // 3 A1|3 // 229055 ///	Zbtb10	0.000133695	2.06786
NM_011313 // S100a6 // S100 calcium binding protein A6 (calcyclin) // 3 F1-F2|3 39.35 c	S100a6	7.23E-05	2.06768
ENSMUST00000173858 // Efr3a // EFR3 homolog A (S. cerevisiae) // 15 D1|15 // 76740 ///	Efr3a	0.000197226	2.06501
NM_026570 // Yeats4 // YEATS domain containing 4 // 10 D2|10 // 64050 /// ENSMUST000000	Yeats4	6.65E-05	2.06486
NM_030697 // Kank3 // KN motif and ankyrin repeat domains 3 // 17 B1|17 17.98 cM // 808	Kank3	0.000506218	2.06293
NR_037666 // Gm16861 // predicted gene, 16861 // 16|16 2.48 cM // 100503704 /// ENSMUST	Gm16861	0.00027841	2.06042
NM_008873 // Plau // plasminogen activator, urokinase // 14 A3|14 11.53 cM // 18792 ///	Plau	5.46E-05	2.06007
NM_019438 // Ncapg // non-SMC condensin I complex, subunit G // 5 B3|5 // 54392 /// XR_	Ncapg	0.00503321	2.05957
NM_007459 // Ap2a2 // adaptor-related protein complex 2, alpha 2 subunit // 7 F5|7 // 1	Ap2a2	3.28E-07	2.05808
NM_001033336 // Abcc4 // ATP-binding cassette, sub-family C (CFTR/MRP), member 4 // 14	Abcc4	0.000107389	2.05617
NM_013935 // Ptpla // protein tyrosine phosphatase-like (proline instead of catalytic a	Ptpla	0.000241228	2.05583
XR_388930 // LOC102635561 // uncharacterized LOC102635561 // --- // 102635561 /// XR_39	LOC102635561	0.000177537	2.05579
---		0.000832334	2.05465
NM_001081238 // Palb2 // partner and localizer of BRCA2 // 7 F3|7 // 233826 /// ENSMUST	Palb2	0.00316914	2.05431
ENSMUST00000105868 // Stmn1 // stathmin 1 // 4 D3|4 66.76 cM // 16765 /// NM_019641 //	Stmn1	0.00167382	2.05344
XM_006516362 // Nubpl // nucleotide binding protein-like // 12 C1|12 // 76826 /// XM_00	Nubpl	0.00349325	2.05301
---		0.000966077	2.05243
NM_001159572 // 4632428N05Rik // RIKEN cDNA 4632428N05 gene // 10 B4|10 // 74048 /// NM	4632428N05Rik	4.44E-06	2.0524
NM_029600 // Abcc3 // ATP-binding cassette, sub-family C (CFTR/MRP), member 3 // 11 D|1	Abcc3	4.74E-07	2.052
NM_029938 // H2afv // H2A histone family, member V // 11 A1|11 // 77605 /// ENSMUST0000	H2afv	0.00057191	2.05185
NM_138753 // Hexim1 // hexamethylene bis-acetamide inducible 1 // 11 E1|11 // 192231 //	Hexim1	2.71E-05	2.0501
NM_029492 // Zdhhc20 // zinc finger, DHHC domain containing 20 // 14 C3|14 // 75965 ///	Zdhhc20	8.08E-05	2.04974
NM_146261 // Fam199x // family with sequence similarity 199, X-linked // X F1|X // 2456	Fam199x	0.000240685	2.04778
AK131743 // Gm10572 // predicted gene 10572 // 4 D2.2|4 // 100038647	Gm10572	0.00122065	2.04759
ENSMUST00000183421 // Trps1 // trichorhinophalangeal syndrome I (human) // 15 C|15 19.1	Trps1	9.40E-05	2.04729
NM_181584 // Gab3 // growth factor receptor bound protein 2-associated protein 3 // X A	Gab3	0.00113524	2.04721
NM_019993 // Aldh9a1 // aldehyde dehydrogenase 9, subfamily A1 // 1|1 H2 // 56752 /// X	Aldh9a1	5.95E-06	2.04414
ENSMUST00000083297 // Gm22972 // predicted gene, 22972 // --- // --- /// ENSMUST0000014	Gm22972	2.00E-05	2.04372
---		0.00445071	2.04366
NM_009149 // Glg1 // golgi apparatus protein 1 // 8 E1|8 57.98 cM // 20340 /// ENSMUST0	Glg1	1.01E-05	2.04322
NM_001081212 // Irs2 // insulin receptor substrate 2 // 8 A1.1|8 5.35 cM // 384783 ///	Irs2	0.00258127	2.04278
---		0.000156326	2.04267
NM_001285463 // Carf // calcium response factor // 1 C2|1 // 241066 /// NM_001285473 //	Carf	0.00152926	2.04243
NM_153587 // Rps6ka5 // ribosomal protein S6 kinase, polypeptide 5 // 12 E|12 // 73086	Rps6ka5	0.000855821	2.04236
NM_172700 // Zmpste24 // zinc metallopeptidase, STE24 // 4 D2.2|4 // 230709 /// ENSMUST	Zmpste24	9.34E-05	2.04188
NM_027188 // Smyd3 // SET and MYND domain containing 3 // 1 H3|1 83.48 cM // 69726 ///	Smyd3	8.05E-05	2.04172
---		0.0024524	2.04133
NM_001164624 // Zfp809 // zinc finger protein 809 // 9 A3|9 // 235047 /// NM_172763 //	Zfp809	0.000157616	2.04074
NM_011035 // Pak1 // p21 protein (Cdc42/Rac)-activated kinase 1 // 7 E2|7 53.57 cM // 1	Pak1	7.95E-06	2.04073
NM_007790 // Smc3 // structural maintenance of chromosomes 3 // 19 D2|19 // 13006 /// E	Smc3	4.71E-06	2.04009
NM_027810 // Bbs7 // Bardet-Biedl syndrome 7 (human) // 3 B|3 // 71492 /// ENSMUST00000	Bbs7	0.000341261	2.03995
NM_026189 // Eepd1 // endonuclease/exonuclease/phosphatase family domain containing 1 /	Eepd1	5.90E-05	2.03723
NM_019549 // Plek // pleckstrin // 11 A2|11 9.41 cM // 56193 /// ENSMUST00000102881 //	Plek	0.000337069	2.03672
NM_026174 // Entpd4 // ectonucleoside triphosphate diphosphohydrolase 4 // 14 D2|14 //	Entpd4	1.37E-08	2.03542
NM_207659 // Hook3 // hook homolog 3 (Drosophila) // 8 A2|8 // 320191 /// XM_006509149	Hook3	1.03E-06	2.03449
NM_026796 // Smyd2 // SET and MYND domain containing 2 // 1 H6|1 // 226830 /// XM_00649	Smyd2	0.000564274	2.03372
ENSMUST00000082411 // ND3 // NADH dehydrogenase subunit 3 // --- // 17718 /// AK139029	ND3	6.43E-06	2.03307
NM_178143 // Prkaa2 // protein kinase, AMP-activated, alpha 2 catalytic subunit // 4 C6	Prkaa2	0.000310474	2.03078
NM_025863 // Trim59 // tripartite motif-containing 59 // 3|3 E2 // 66949 /// ENSMUST000	Trim59	0.00106218	2.02981
NM_145456 // Zswim6 // zinc finger SWIM-type containing 6 // 13 D2.1|13 // 67263 /// EN	Zswim6	9.32E-05	2.02917
ENSMUST00000041659 // Prrx2 // paired related homeobox 2 // 2 B|2 21.74 cM // 20204 ///	Prrx2	0.000396742	2.02907
NM_025693 // Tmem41a // transmembrane protein 41a // 16 B1|16 // 66664 /// NR_037773 //	Tmem41a	0.000616502	2.0285
NM_001164503 // Akap11 // A kinase (PRKA) anchor protein 11 // 14 D3|14 // 219181 /// E	Akap11	0.000427388	2.02706
NM_199198 // Hdac10 // histone deacetylase 10 // 15 E3|15 // 170787 /// NR_028447 // Hd	Hdac10	0.00235608	2.02685
NM_008212 // Hadh // hydroxyacyl-Coenzyme A dehydrogenase // 3 G3|3 // 15107 /// ENSMUS	Hadh	9.38E-05	2.02643
NR_046048 // Gm10677 // predicted gene 10677 // --- // 100038460	Gm10677	0.00030983	2.0257
NM_001038621 // Rabgap1l // RAB GTPase activating protein 1-like // 1 H2.1|1 // 29809 /	Rabgap1l	0.000597479	2.02533
NM_001205369 // Casc4 // cancer susceptibility candidate 4 // 2 E5|2 // 319996 /// NM_0	Casc4	0.00496106	2.02116
NM_008021 // Foxm1 // forkhead box M1 // 6 F3|6 62.98 cM // 14235 /// ENSMUST0000007331	Foxm1	0.00190442	2.01964
NM_080288 // Elmo1 // engulfment and cell motility 1 // 13|13 A3.1 // 140580 /// NM_198	Elmo1	1.14E-05	2.01922
XR_374487 // Knstrn // kinetochore-localized astrin/SPAG5 binding // 2 E5|2 // 51944 //	Knstrn	0.00031995	2.01769
NM_029306 // 1700012B09Rik // RIKEN cDNA 1700012B09 gene // 9 A2|9 // 69325 /// XR_3791	1700012B09Rik	0.00140795	2.01518
NR_040556 // Gm6634 // predicted gene 6634 // 3 E2|3 // 625901 /// ENSMUST00000180497 /	Gm6634	0.000704484	2.01508
NM_001083334 // Bin1 // bridging integrator 1 // 18 B1|18 18.01 cM // 30948 /// NM_0096	Bin1	3.97E-06	2.01466
---		0.000636952	2.01316
NM_009796 // Capn7 // calpain 7 // 14 B|14 // 12339 /// ENSMUST00000022451 // Capn7 //	Capn7	2.79E-05	2.01188
NM_001033155 // Dnajb14 // DnaJ (Hsp40) homolog, subfamily B, member 14 // 3 G3|3 // 70	Dnajb14	4.30E-06	2.01173
ENSMUST00000112103 // Nav1 // neuron navigator 1 // --- // --- /// AK158038 // Nav1 //	Nav1	0.00522844	2.01147
NM_001015681 // E130308A19Rik // RIKEN cDNA E130308A19 gene // 4 B3|4 // 230259 /// NM_	E130308A19Rik	0.000637824	2.01105
NM_011992 // Rcn2 // reticulocalbin 2 // 9|9 C // 26611 /// ENSMUST00000114276 // Rcn2	Rcn2	8.17E-07	2.00982
NM_001110195 // Echdc1 // enoyl Coenzyme A hydratase domain containing 1 // 10 A4|10 16	Echdc1	0.000103404	2.00971
NM_028320 // Adipor1 // adiponectin receptor 1 // 1 E4|1 // 72674 /// ENSMUST0000002772	Adipor1	1.77E-06	2.00947

ENSMUST00000148876 // Mettl8 // methyltransferase like 8 // 2 C2|2 // 228019 /// NM_001	Mettl8	0.00105169	2.00934
NM_008961 // Pter // phosphotriesterase related // 2 A1|2 // 19212 /// XM_006497400 //	Pter	0.000458353	2.00876
NM_008737 // Nrp1 // neuropilin 1 // 8 E|8 75.78 cM // 18186 /// ENSMUST00000026917 //	Nrp1	1.64E-05	2.00795
NR_045008 // Gm20300 // predicted gene, 20300 // 10|10 17.1 cM // 100504586	Gm20300	0.00363361	2.00788
NM_011218 // Ptprs // protein tyrosine phosphatase, receptor type, S // 17 D|17 29.32 c	Ptprs	0.00193437	2.00758
NM_010499 // Ier2 // immediate early response 2 // 8 C3|8 41.02 cM // 15936 /// ENSMUST	Ier2	8.59E-06	2.00626
NM_144918 // Smyd5 // SET and MYND domain containing 5 // 6 C3|6 37.44 cM // 232187 ///	Smyd5	2.40E-05	2.00593
NM_199476 // Rrm2b // ribonucleotide reductase M2 B (TP53 inducible) // 15 B3.1|15 // 3	Rrm2b	0.000136839	2.00529
NM_011623 // Top2a // topoisomerase (DNA) II alpha // 11 D|11 62.91 cM // 21973 /// ENS	Top2a	6.10E-05	2.00525
NM_153153 // Svil // supervillin // 18 A1|18 // 225115 /// XM_006525793 // Svil // supe	Svil	0.000429031	2.00512
NM_001076789 // Cbx5 // chromobox 5 // 15 F3|15 // 12419 /// NM_001110216 // Cbx5 // ch	Cbx5	3.46E-05	2.00408
NM_001159365 // Cep97 // centrosomal protein 97 // 16 C1.1|16 // 74201 /// NM_001159366	Cep97	0.00233242	2.00377
NM_133829 // Mfsd6 // major facilitator superfamily domain containing 6 // 1 C1.1|1 //	Mfsd6	9.11E-05	2.00248
NR_015585 // 4933439C10Rik // RIKEN cDNA 4933439C10 gene // 11 B1.3|11 // 74476 /// ENS	4933439C10Rik	0.00080427	2.00238
NM_144877 // Mettl13 // methyltransferase like 13 // 1|1 H1 // 71449 /// ENSMUST0000002	Mettl13	0.00299739	2.00049
NM_001167883 // Ankrd50 // ankyrin repeat domain 50 // 3 B|3 // 99696 /// ENSMUST000001	Ankrd50	1.49E-05	-2.00037
NM_001048054 // Dusp16 // dual specificity phosphatase 16 // 6 G1|6 65.77 cM // 70686 /	Dusp16	0.00037141	-2.00129
NM_013562 // Ifrd1 // interferon-related developmental regulator 1 // 12 B1|12 18.06 cM	Ifrd1	3.23E-05	-2.00175
NM_021449 // Crbn // cereblon // 6 E2|6 // 58799 /// NM_175357 // Crbn // cereblon // 6	Crbn	5.64E-07	-2.00461
---		0.0040079	-2.0055
NM_031257 // Plekha2 // pleckstrin homology domain-containing, family A (phosphoinositi	Plekha2	7.01E-06	-2.00581
NM_015797 // Fbxo6 // F-box protein 6 // 4 E2|4 78.67 cM // 50762 /// ENSMUST0000010570	Fbxo6	3.38E-05	-2.00631
NM_175687 // A230050P20Rik // RIKEN cDNA A230050P20 gene // 9 A3|9 // 319278 /// ENSMUS	A230050P20Rik	0.000660084	-2.00667
NM_133816 // Sh3bp4 // SH3-domain binding protein 4 // 1 D|1 // 98402 /// ENSMUST000000	Sh3bp4	0.000437284	-2.0073
NM_054041 // Antxr1 // anthrax toxin receptor 1 // 6 D1|6 // 69538 /// XM_006506564 //	Antxr1	3.56E-06	-2.00761
NM_025653 // 3110001I22Rik // RIKEN cDNA 3110001I22 gene // 16 A1|16 // 66598 /// NM_02	3110001I22Rik	5.52E-05	-2.01109
NM_001077684 // Ccdc173 // coiled-coil domain containing 173 // 2 C2|2 // 75051 /// ENS	Ccdc173	0.000997558	-2.01157
---		3.86E-05	-2.01202
---		0.00135178	-2.01526
NM_001039103 // Rasa4 // RAS p21 protein activator 4 // 5 G2|5 // 54153 /// NM_133914 /	Rasa4	0.000139785	-2.01725
ENSMUST00000103694 // Traj49 // T cell receptor alpha joining 49 // --- // --- /// AK13	Traj49	0.000807816	-2.01729
ENSMUST00000015812 // Pdzd11 // PDZ domain containing 11 // X C3|X // 72621 /// ENSMUST	Pdzd11	6.61E-05	-2.02023
NM_009401 // Tnfrsf8 // tumor necrosis factor receptor superfamily, member 8 // 4 E1|4	Tnfrsf8	0.00501895	-2.02059
XR_380941 // LOC102633407 // uncharacterized LOC102633407 // --- // 102633407 /// ENSMU	LOC102633407	0.000175127	-2.02143
NM_001291003 // Astl // astacin-like metalloendopeptidase (M12 family) // 2|2 F // 2150	Astl	0.000161339	-2.02154
NM_001291358 // Pgap2 // post-GPI attachment to proteins 2 // 7 E3|7 // 233575 /// NM_1	Pgap2	1.53E-05	-2.0221
---		0.000207731	-2.02329
NM_001201341 // Msi2 // musashi RNA-binding protein 2 // 11 C|11 // 76626 /// NM_054043	Msi2	0.000463308	-2.02419
NM_145584 // Spon1 // spondin 1, (f-spondin) extracellular matrix protein // 7 F1|7 //	Spon1	0.00126488	-2.02523
NM_019788 // Bloc1s6 // biogenesis of lysosomal organelles complex-1, subunit 6, pallid	Bloc1s6	4.03E-05	-2.02703
NM_001098789 // Ndufa4l2 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like	Ndufa4l2	0.0025229	-2.02808
NM_001163430 // Sirt6 // sirtuin 6 // 10 C1|10 39.72 cM // 50721 /// XM_006513861 // Si	Sirt6	0.000743268	-2.03189
ENSMUST00000122606 // Gm25270 // predicted gene, 25270 // --- // ---	Gm25270	0.000351397	-2.03268
NM_001277255 // Acvrl1 // activin A receptor, type II-like 1 // 15|15 F3 // 11482 /// N	Acvrl1	8.16E-06	-2.03454
ENSMUST00000171380 // Gm17337 // predicted gene, 17337 // --- // ---	Gm17337	0.000603382	-2.03645
NM_197986 // Tmem140 // transmembrane protein 140 // 6 B1|6 // 68487 /// XM_006506540 /	Tmem140	2.46E-06	-2.03757
NM_007808 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063 /// ENSMUST000	Cycs	0.00129803	-2.03764
NM_007808 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063 /// ENSMUST000	Cycs	0.00129803	-2.03764
NM_001025313 // Tapbp // TAP binding protein // 17 B1|17 17.98 cM // 21356 /// NM_00931	Tapbp	1.96E-05	-2.03881
NM_001252593 // Cars // cysteinyl-tRNA synthetase // 7 F5|7 88.25 cM // 27267 /// NM_01	Cars	0.000165959	-2.03997
NM_001002005 // Panx2 // pannexin 2 // 15E3|15 // 406218 /// XM_006521139 // Panx2 // p	Panx2	4.63E-05	-2.04156
NM_001252503 // Aftph // aftiphilin // 11 A3.1|11 // 216549 /// NM_001290545 // Aftph /	Aftph	0.000305871	-2.04182
NM_001190817 // Dnajc1 // DnaJ (Hsp40) homolog, subfamily C, member 1 // 2|2 A2 // 1341	Dnajc1	0.000134747	-2.04389
NM_153570 // Noc4l // nucleolar complex associated 4 homolog (S. cerevisiae) // 5 F|5 /	Noc4l	4.95E-08	-2.04495
NM_011596 // Atp6v0a2 // ATPase, H+ transporting, lysosomal V0 subunit A2 // 5 F|5 // 2	Atp6v0a2	1.94E-08	-2.04641
NM_001033534 // Layn // layilin // 9 A5.3|9 // 244864 /// ENSMUST00000098782 // Layn //	Layn	1.21E-05	-2.04676
NM_011581 // Thbs2 // thrombospondin 2 // 17 A3-B|17 8.95 cM // 21826 /// ENSMUST000001	Thbs2	0.00256675	-2.04711
ENSMUST00000180613 // Gdap10 // ganglioside-induced differentiation-associated-protein	Gdap10	0.00015915	-2.04821
NM_001081175 // Itpkb // inositol 1,4,5-trisphosphate 3-kinase B // 1 H5|1 84.27 cM //	Itpkb	4.96E-06	-2.0484
NM_008480 // Lama1 // laminin, alpha 1 // 17 E1.1|17 38.8 cM // 16772 /// ENSMUST000000	Lama1	0.00204748	-2.04967
---		0.00266243	-2.05087
NM_001113326 // Msr1 // macrophage scavenger receptor 1 // 8 A4|8 23.89 cM // 20288 ///	Msr1	1.16E-05	-2.05358
NM_009744 // Bcl6 // B cell leukemia/lymphoma 6 // 16 B1|16 15.26 cM // 12053 /// ENSMU	Bcl6	2.08E-06	-2.05522
NM_028132 // Pgm2 // phosphoglucomutase 2 // 4 C6|4 45.71 cM // 72157 /// ENSMUST000000	Pgm2	2.25E-05	-2.06347
NM_201518 // Flrt2 // fibronectin leucine rich transmembrane protein 2 // 12 E|12 // 39	Flrt2	2.91E-05	-2.06362
NR_040335 // D330050G23Rik // RIKEN cDNA D330050G23 gene // 2|2 // 320975 /// ENSMUST00	D330050G23Rik	0.000382936	-2.06404
NM_008826 // Pfkl // phosphofructokinase, liver, B-type // 10 C1|10 39.72 cM // 18641 /	Pfkl	6.93E-06	-2.06639
NM_175175 // Plekhf2 // pleckstrin homology domain containing, family F (with FYVE doma	Plekhf2	9.41E-06	-2.06807
NM_026968 // Manbal // mannosidase, beta A, lysosomal-like // 2 H1|2 // 69161 /// ENSMU	Manbal	2.77E-05	-2.0698
ENSMUST00000101800 // Msrb1 // methionine sulfoxide reductase B1 // 17 A3.3|17 12.53 cM	Msrb1	0.000746314	-2.07036
NM_011016 // Orm2 // orosomucoid 2 // 4 C1|4 33.96 cM // 18406 /// ENSMUST00000075341 /	Orm2	0.00345026	-2.07058
---		1.67E-05	-2.07229
NM_207636 // Fndc3a // fibronectin type III domain containing 3A // 14 D2|14 37.62 cM /	Fndc3a	3.78E-05	-2.07419
NM_144522 // Tbc1d10b // TBC1 domain family, member 10b // 7|7 F4 // 68449 /// ENSMUST0	Tbc1d10b	0.000101801	-2.07449
NM_001142809 // Slc6a8 // solute carrier family 6 (neurotransmitter transporter, creati	Slc6a8	6.38E-08	-2.07514
NM_009447 // Tuba4a // tubulin, alpha 4A // 1|1 C3 // 22145 /// ENSMUST00000079464 // T	Tuba4a	6.92E-05	-2.07633
NM_001145858 // Sh3bp2 // SH3-domain binding protein 2 // 5 B2|5 // 24055 /// NM_001145	Sh3bp2	6.01E-06	-2.07641
---		0.00100118	-2.07684
NM_177607 // 4933430I17Rik // RIKEN cDNA 4933430I17 gene // 4 B3|4 // 214106 /// ENSMUS	4933430I17Rik	0.00185415	-2.07808
NM_007793 // Cstb // cystatin B // 10 C1|10 39.72 cM // 13014 /// ENSMUST00000005185 //	Cstb	0.000156285	-2.07975
---		0.000499137	-2.08044
NM_010907 // Nfkbia // nuclear factor of kappa light polypeptide gene enhancer in B cel	Nfkbia	0.000869502	-2.0823
NM_001111279 // Wdfy1 // WD repeat and FYVE domain containing 1 // 1|1 C4 // 69368 ///	Wdfy1	0.00363192	-2.08417
NM_198642 // 5031414D18Rik // RIKEN cDNA 5031414D18 gene // 14 D3|14 // 271221 /// ENSM	5031414D18Rik	0.00094129	-2.08451
ENSMUST00000135573 // Gm21399 // peroxiredoxin 1 pseudogene // 8|8 // 100862012 /// ENS	Gm21399	1.32E-05	-2.08642
ENSMUST00000101295 // 9930111J21Rik2 // RIKEN cDNA 9930111J21 gene 2 // 11 B1.2|11 // 2	9930111J21Rik	0.00356031	-2.08652
NM_172428 // Ccdc134 // coiled-coil domain containing 134 // 15 E1|15 // 76457 /// XM_0	Ccdc134	0.000487045	-2.08729
NM_001145935 // Zfp691 // zinc finger protein 691 // 4 D2.1|4 // 195522 /// NM_183140 /	Zfp691	0.000149571	-2.08765
NM_198007 // Ascc3 // activating signal cointegrator 1 complex subunit 3 // 10 B3|10 //	Ascc3	0.000304546	-2.08949

NM_001113569 // Stxbp1 // syntaxin binding protein 1 // 2 B|2 22.09 cM // 20910 /// NM_	Stxbp1	0.000135617	-2.08951
NM_013566 // Itgb7 // integrin beta 7 // 15 F3|15 57.39 cM // 16421 /// ENSMUST00000001	Itgb7	0.000553297	-2.09165
NM_008591 // Met // met proto-oncogene // 6 A2|6 7.83 cM // 17295 /// ENSMUST0000011544	Met	0.0023217	-2.09308
NM_033601 // Bcl3 // B cell leukemia/lymphoma 3 // 7 A3|7 9.95 cM // 12051 /// ENSMUST0	Bcl3	0.000295204	-2.09505
NM_019631 // Tmem45a // transmembrane protein 45a // 16 C1.1|16 // 56277 /// XM_0065223	Tmem45a	7.00E-06	-2.09581
NM_011851 // Nt5e // 5 nucleotidase, ecto // 9|9 E3.2 // 23959 /// ENSMUST00000034992 /	Nt5e	9.51E-06	-2.09696
NR_038038 // Hk1os // hexokinase 1, opposite strand // 10 B4|10 // 70162 /// ENSMUST000	Hk1os	0.00248913	-2.10056
NM_175529 // Leng9 // leukocyte receptor cluster (LRC) member 9 // 7 A1|7 // 243813 ///	Leng9	0.00187146	-2.10084
---		0.00373139	-2.10306
NM_013605 // Muc1 // mucin 1, transmembrane // 3 F1|3 39.02 cM // 17829 /// ENSMUST0000	Muc1	0.00269169	-2.1039
NM_013712 // Itgb1bp2 // integrin beta 1 binding protein 2 // X|X D // 26549 /// ENSMUS	Itgb1bp2	0.00151829	-2.10402
NM_153422 // Pde5a // phosphodiesterase 5A, cGMP-specific // 3 G1|3 // 242202 /// XM_00	Pde5a	0.00180104	-2.10507
ENSMUST00000080062 // Gm17541 // predicted gene, 17541 // --- // ---	Gm17541	0.000333621	-2.10542
NM_175523 // Ppm1k // protein phosphatase 1K (PP2C domain containing) // 6 B3|6 // 2433	Ppm1k	0.00130113	-2.10762
---		0.00417487	-2.10891
ENSMUST00000152813 // Spata5l1 // spermatogenesis associated 5-like 1 // --- // --- ///	Spata5l1	0.00217273	-2.10923
NM_025427 // Rgcc // regulator of cell cycle // 14 D3|14 // 66214 /// XM_006519373 // R	Rgcc	0.00184856	-2.10953
ENSMUST00000092990 // Agpat9 // 1-acylglycerol-3-phosphate O-acyltransferase 9 // 5 E4|	Agpat9	0.00116135	-2.11094
---		0.00168847	-2.11138
NM_146893 // Olfr1216 // olfactory receptor 1216 // 2 E1|2 // 258895 /// ENSMUST0000009	Olfr1216	0.00116615	-2.11186
NM_001114679 // 9930111J21Rik1 // RIKEN cDNA 9930111J21 gene 1 // 11 B1.2|11 // 667214	9930111J21Rik	0.000547307	-2.11421
NM_001024474 // Diras2 // DIRAS family, GTP-binding RAS-like 2 // 13 A5|13 // 68203 ///	Diras2	0.00126303	-2.11447
NM_130864 // Acaa1a // acetyl-Coenzyme A acyltransferase 1A // 9 F4|9 71.33 cM // 11386	Acaa1a	0.00234895	-2.11497
NM_133501 // Ntng2 // netrin G2 // 2 B|2 19.57 cM // 171171 /// ENSMUST00000048455 // N	Ntng2	0.000910265	-2.11714
NM_020042 // Mocs1 // molybdenum cofactor synthesis 1 // 17 C|17 // 56738 /// NM_028464	Mocs1	0.000533857	-2.11881
NM_016846 // Rgl1 // ral guanine nucleotide dissociation stimulator,-like 1 // 1|1 G2 /	Rgl1	0.000312751	-2.12013
NM_029338 // Rsph9 // radial spoke head 9 homolog (Chlamydomonas) // 17|17 C // 75564 /	Rsph9	0.00367718	-2.12095
ENSMUST00000100700 // Gm10382 // predicted gene 10382 // --- // --- /// AK132914 // Gm1	Gm10382	0.00102916	-2.1233
---		0.000379934	-2.12619
XM_006530180 // Msi1 // musashi RNA-binding protein 1 // 5 E3-F|5 // 17690 /// ENSMUST0	Msi1	0.00296668	-2.12641
---		0.00307879	-2.12813
NM_173386 // Mb21d1 // Mab-21 domain containing 1 // 9 E1|9 // 214763 /// ENSMUST000000	Mb21d1	0.00367549	-2.12917
ENSMUST00000160445 // Gm16549 // predicted gene 16549 // --- // --- /// AK007062 // Fnd	Gm16549	0.000443703	-2.13071
NM_019811 // Acss2 // acyl-CoA synthetase short-chain family member 2 // 2|2 H2 // 6052	Acss2	1.78E-06	-2.13268
ENSMUST00000094754 // Rpl7a-ps8 // ribosomal protein L7A, pseudogene 8 // --- // ---	Rpl7a-ps8	0.00345387	-2.13327
NM_013491 // Clcn1 // chloride channel 1 // 6 B2.1|6 20.57 cM // 12723 /// ENSMUST00000	Clcn1	0.00376894	-2.14275
NM_010870 // Naip5 // NLR family, apoptosis inhibitory protein 5 // 13 D1|13 53.05 cM /	Naip5	2.25E-05	-2.145
ENSMUST00000071792 // 1110038F14Rik // RIKEN cDNA 1110038F14 gene // 15|15 E1 // 117171	1110038F14Rik	0.000106131	-2.14511
NM_023247 // Ndufaf3 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly fa	Ndufaf3	0.000161913	-2.14513
NM_031406 // Slc12a9 // solute carrier family 12 (potassium/chloride transporters), mem	Slc12a9	0.00017598	-2.14522
NM_001252550 // BC017643 // cDNA sequence BC017643 // 11 E2|11 // 217370 /// NM_0012547	BC017643	1.23E-06	-2.14536
NM_020497 // Zfp276 // zinc finger protein (C2H2 type) 276 // 8 E1|8 72.09 cM // 57247	Zfp276	0.000340053	-2.14634
ENSMUST00000106854 // Trim34a // tripartite motif-containing 34A // 7|7 F1 // 94094	Trim34a	0.000965647	-2.14696
NM_153805 // Pkn3 // protein kinase N3 // 2 B|2 // 263803 /// XM_006498052 // Pkn3 // p	Pkn3	5.78E-05	-2.14825
XM_006542015 // LOC102635000 // uncharacterized LOC102635000 // --- // 102635000 /// XM	LOC102635000	0.00330601	-2.15012
NM_008869 // Pla2g4a // phospholipase A2, group IVA (cytosolic, calcium-dependent) // 1	Pla2g4a	0.00238013	-2.15408
NM_021355 // Fmod // fibromodulin // 1 E4|1 58.09 cM // 14264 /// ENSMUST00000048183 //	Fmod	0.00156579	-2.1545
NM_199322 // Dot1l // DOT1-like, histone H3 methyltransferase (S. cerevisiae) // 10 C1|	Dot1l	3.79E-05	-2.15461
NM_027450 // Glipr2 // GLI pathogenesis-related 2 // 4 B1|4 // 384009 /// ENSMUST000000	Glipr2	0.000835073	-2.15501
NM_028451 // Larp1 // La ribonucleoprotein domain family, member 1 // 11|11 B2 // 73158	Larp1	0.000112722	-2.15504
NM_023168 // Grina // glutamate receptor, ionotropic, N-methyl D-aspartate-associated p	Grina	2.13E-06	-2.15531
NM_001177843 // Frmd4a // FERM domain containing 4A // 2 A1|2 // 209630 /// NM_172475 /	Frmd4a	6.38E-06	-2.15536
NM_027334 // Mettl7a1 // methyltransferase like 7A1 // 15|15 F3 // 70152 /// XM_0065213	Mettl7a1	0.000203274	-2.15623
NM_175013 // Pgm5 // phosphoglucomutase 5 // 19 B|19 // 226041 /// ENSMUST00000047666 /	Pgm5	0.000154963	-2.15645
NM_019932 // Pf4 // platelet factor 4 // 5 E1|5 // 56744 /// ENSMUST00000031320 // Pf4	Pf4	0.00122957	-2.15697
ENSMUST00000105015 // Gm14347 // predicted gene 14347 // X A1.1|X // 627264	Gm14347	0.00366025	-2.15796
ENSMUST00000157928 // Gm22101 // predicted gene, 22101 // --- // ---	Gm22101	0.00149944	-2.15933
NM_153583 // Atg4d // autophagy related 4D, cysteine peptidase // 9 A3|9 // 235040 ///	Atg4d	0.000645001	-2.16203
NM_007413 // Adora2b // adenosine A2b receptor // 11 B2|11 // 11541 /// ENSMUST00000018	Adora2b	0.00369613	-2.16409
ENSMUST00000034522 // Clmp // CXADR-like membrane protein // 9 A5.1|9 // 71566 /// NM_1	Clmp	2.39E-11	-2.16549
NM_001290667 // Chac2 // ChaC, cation transport regulator 2 // 11 A4|11 // 68044 /// NM	Chac2	0.00245236	-2.1655
---		0.00152773	-2.16699
NM_025286 // Slc31a2 // solute carrier family 31, member 2 // 4 B3|4 // 20530 /// ENSMU	Slc31a2	0.000125318	-2.16726
AK136930 // Gm4583 // predicted gene 4583 // 14 D1|14 // 100043676	Gm4583	0.00486052	-2.17333
NM_011400 // Slc2a1 // solute carrier family 2 (facilitated glucose transporter), membe	Slc2a1	8.00E-06	-2.17518
---		0.00365395	-2.17674
NM_033622 // Tnfsf13b // tumor necrosis factor (ligand) superfamily, member 13b // 8 A1	Tnfsf13b	0.000131607	-2.18635
NM_013790 // Abcc5 // ATP-binding cassette, sub-family C (CFTR/MRP), member 5 // 16 A3|	Abcc5	1.27E-05	-2.18771
NM_001080926 // Lrp8 // low density lipoprotein receptor-related protein 8, apolipoprot	Lrp8	2.31E-06	-2.18776
NM_001289704 // Cflar // CASP8 and FADD-like apoptosis regulator // 1 C1.3|1 29.16 cM /	Cflar	0.00365715	-2.18811
NM_011174 // Prh1 // proline rich protein HaeIII subfamily 1 // 6 G1|6 64.03 cM // 1913	Prh1	0.000112794	-2.18921
NM_009450 // Tubb2a // tubulin, beta 2A class IIA // 13 A3.3|13 14.03 cM // 22151 /// E	Tubb2a	9.49E-06	-2.19402
NM_009410 // Top3a // topoisomerase (DNA) III alpha // 11 B2|11 // 21975 /// ENSMUST000	Top3a	0.000596338	-2.1945
NM_026438 // Ppa1 // pyrophosphatase (inorganic) 1 // 10 B4|10 32.25 cM // 67895 /// EN	Ppa1	5.47E-06	-2.1947
NM_001168684 // Tmcc3 // transmembrane and coiled coil domains 3 // 10 C2|10 // 319880	Tmcc3	0.00107634	-2.19602
NM_011186 // Psmb5 // proteasome (prosome, macropain) subunit, beta type 5 // 14 C2-D1|	Psmb5	3.23E-06	-2.19681
NM_010172 // F7 // coagulation factor VII // 8 A1.1|8 5.73 cM // 14068 /// ENSMUST00000	F7	1.87E-06	-2.19724
NM_007909 // Efna2 // ephrin A2 // 10 C1|10 39.72 cM // 13637 /// ENSMUST00000003154 //	Efna2	0.00226483	-2.19935
NR_073569 // Klrb1-ps1 // killer cell lectin-like receptor subfamily B member 1, pseudo	Klrb1-ps1	0.0050933	-2.20314
ENSMUST00000067924 // Lrrc8c // leucine rich repeat containing 8 family, member C // 5	Lrrc8c	7.37E-05	-2.20326
NM_001037762 // Zdhhc12 // zinc finger, DHHC domain containing 12 // 2 B|2 // 66220 ///	Zdhhc12	0.000118297	-2.20356
NM_007808 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063 /// ENSMUST000	Cycs	0.000129559	-2.20416
NM_178796 // A530064D06Rik // RIKEN cDNA A530064D06 gene // 17 C|17 // 328830 /// ENSMU	A530064D06Ril	4.61E-05	-2.20715
ENSMUST00000145961 // Gm12764 // predicted gene 12764 // --- // ---	Gm12764	0.000876045	-2.20885
NM_009393 // Tnnc1 // troponin C, cardiac/slow skeletal // 14 B|14 19.09 cM // 21924 //	Tnnc1	0.00172835	-2.21409
---		2.47E-06	-2.21453
NM_177876 // Vps37b // vacuolar protein sorting 37B (yeast) // 5 F|5 // 330192 /// ENSM	Vps37b	0.00137714	-2.21571
NM_183426 // Sbno2 // strawberry notch homolog 2 (Drosophila) // 10 C1|10 // 216161 ///	Sbno2	5.00E-07	-2.21628
---		0.000560039	-2.21812

NM_023044 // Slc15a3 // solute carrier family 15, member 3 // 19|19 B // 65221 /// ENSM	Slc15a3	2.12E-05	-2.22241
NM_172733 // Dera // 2-deoxyribose-5-phosphate aldolase homolog (C. elegans) // 6 G1|6	Dera	3.10E-06	-2.22482
---		0.000401391	-2.2271
ENSMUST00000180468 // Gm26510 // predicted gene, 26510 // --- // --- /// XR_397622 // L	Gm26510	0.00113077	-2.22719
NM_007802 // Ctsk // cathepsin K // 3 F2.1|3 40.74 cM // 13038 /// ENSMUST00000015664 /	Ctsk	0.0011834	-2.23075
NR_045687 // Gm9895 // predicted gene 9895 // 19 C1|19 // 100503337	Gm9895	0.000386221	-2.23188
NM_008851 // Pitpnm1 // phosphatidylinositol transfer protein, membrane-associated 1 //	Pitpnm1	3.78E-06	-2.23632
---		0.000348463	-2.23985
NM_153074 // Lrrc25 // leucine rich repeat containing 25 // 8 B3.3|8 // 211228 /// ENSM	Lrrc25	0.000384073	-2.24163
---		0.000150386	-2.24358
NM_009621 // Adamts1 // a disintegrin-like and metallopeptidase (reprolysin type) with	Adamts1	0.00284844	-2.24463
NM_026073 // Ift22 // intraflagellar transport 22 // 5|5 G1 // 67286 /// ENSMUST0000000	Ift22	2.79E-05	-2.24949
NM_013913 // Angptl3 // angiopoietin-like 3 // 4 C6|4 45.6 cM // 30924 /// ENSMUST00000	Angptl3	0.000100375	-2.25096
NM_028035 // Snx10 // sorting nexin 10 // 6 B3|6 // 71982 /// NM_001127348 // Snx10 //	Snx10	1.86E-05	-2.25102
NM_178892 // Tiparp // TCDD-inducible poly(ADP-ribose) polymerase // 3 E1|3 // 99929 //	Tiparp	9.00E-05	-2.25291
ENSMUST00000027256 // Gm6238 // predicted pseudogene 6238 // X D|X // 621542 /// ENSMUS	Gm6238	0.0012727	-2.25544
NM_027490 // Dcp2 // DCP2 decapping enzyme homolog (S. cerevisiae) // 18 B3|18 // 70640	Dcp2	0.000194515	-2.2562
NM_001284300 // Aifm2 // apoptosis-inducing factor, mitochondrion-associated 2 // 10 B4	Aifm2	4.17E-05	-2.25666
NR_045747 // Gm10872 // predicted gene 10872 // --- // 100038659	Gm10872	0.00243666	-2.25849
---		0.00040573	-2.25855
NM_172652 // Kansl3 // KAT8 regulatory NSL complex subunit 3 // 1 B|1 // 226976 /// XM_	Kansl3	9.46E-06	-2.2597
NM_001159417 // Irf9 // interferon regulatory factor 9 // 14 C3|14 28.19 cM // 16391 //	Irf9	0.000153428	-2.26181
NR_110420 // Ptgs2os2 // prostaglandin-endoperoxide synthase 2, opposite strand 2 // 1	Ptgs2os2	0.00315984	-2.26394
NM_172477 // Dennd2a // DENN/MADD domain containing 2A // 6 B1|6 // 209773 /// XM_00650	Dennd2a	0.00359475	-2.26503
NM_001081684 // Zbtb21 // zinc finger and BTB domain containing 21 // 16|16 C3-4 // 114	Zbtb21	9.24E-05	-2.26536
NM_023422 // Hist1h2bc // histone cluster 1, H2bc // 13 A3.1|13 // 68024 /// ENSMUST000	Hist1h2bc	3.09E-05	-2.26698
NM_001288586 // Mdm2 // transformed mouse 3T3 cell double minute 2 // 10 C1-C3|10 66.32	Mdm2	4.67E-06	-2.26744
NM_009546 // Trim25 // tripartite motif-containing 25 // 11 C|11 // 217069 /// ENSMUST0	Trim25	5.06E-05	-2.26929
ENSMUST00000134427 // Gm11613 // predicted gene 11613 // --- // --- /// AK052674 // LOC	Gm11613	2.97E-05	-2.27133
NM_145478 // Pim3 // proviral integration site 3 // 15 E3|15 // 223775 /// ENSMUST00000	Pim3	0.00132224	-2.27519
NM_027314 // March5 // membrane-associated ring finger (C3HC4) 5 // 19 C2|19 // 69104 /	Mar-05	0.000261791	-2.27614
NR_045304 // 1700030N03Rik // RIKEN cDNA 1700030N03 gene // --- // 70011	1700030N03Rik	0.00276018	-2.27799
NM_172939 // Sowahc // sosondowah ankyrin repeat domain family member C // 10 B4|10 //	Sowahc	5.02E-07	-2.27954
NM_144905 // 6330416G13Rik // RIKEN cDNA 6330416G13 gene // 4 C1|4 // 230279 /// XM_006	6330416G13Rik	8.55E-05	-2.28047
NM_019467 // Aif1 // allograft inflammatory factor 1 // 17 B1|17 18.59 cM // 11629 ///	Aif1	1.76E-05	-2.2811
NM_175326 // D330045A20Rik // RIKEN cDNA D330045A20 gene // X F1|X // 102871 /// ENSMUS	D330045A20Rik	0.00012973	-2.28168
NM_019587 // Plxnb3 // plexin B3 // X A7.3|X // 140571 /// ENSMUST00000002079 // Plxnb3	Plxnb3	0.000268931	-2.2832
NM_021788 // Sap30 // sin3 associated polypeptide // 8 B2|8 29.85 cM // 60406 /// ENSMU	Sap30	2.12E-06	-2.2835
NM_026565 // Apool // apolipoprotein O-like // X|X E2 // 68117 /// XM_006528405 // Apoo	Apool	5.73E-06	-2.28659
NM_001253860 // Scn5a // sodium channel, voltage-gated, type V, alpha // 9 F3-F4|9 71.3	Scn5a	0.000101821	-2.29636
NM_178732 // Zfp324 // zinc finger protein 324 // 7 A1|7 // 243834 /// ENSMUST000000387	Zfp324	0.00225839	-2.29892
NM_145836 // Irf2bpl // interferon regulatory factor 2 binding protein-like // 12 D2|12	Irf2bpl	0.00263065	-2.30053
XM_006505152 // Zfp800 // zinc finger protein 800 // 6 A3.2|6 // 627049 /// ENSMUST0000	Zfp800	5.69E-05	-2.30382
NM_133819 // Ppp1r15b // protein phosphatase 1, regulatory (inhibitor) subunit 15b // 1	Ppp1r15b	4.27E-06	-2.3042
ENSMUST00000171158 // Sdc1 // syndecan 1 // 12 A1.1|12 3.94 cM // 20969 /// ENSMUST0000	Sdc1	1.97E-05	-2.30979
NM_172450 // 4930539E08Rik // RIKEN cDNA 4930539E08 gene // 17 A3.3|17 // 207819 /// EN	4930539E08Rik	0.00265388	-2.31179
XM_006511595 // A730067D02Rik // RIKEN cDNA A730067D02 gene // 9 C|9 // 330963 /// XM_0	A730067D02Rik	0.00100221	-2.31798
NM_001190461 // Hilpda // hypoxia inducible lipid droplet associated // 6 A3.3|6 // 695	Hilpda	3.37E-05	-2.32087
---		4.50E-05	-2.32118
NM_153507 // Cpne2 // copine II // 8 C5|8 // 234577 /// ENSMUST00000048653 // Cpne2 //	Cpne2	9.76E-06	-2.32527
---		0.000957816	-2.32629
NM_016808 // Usp2 // ubiquitin specific peptidase 2 // 9|9 B // 53376 /// NM_198092 //	Usp2	1.42E-05	-2.32737
NM_001290504 // Mid1 // midline 1 // X and Y|X 79.19 cM // 17318 /// NM_001290505 // Mi	Mid1	7.98E-05	-2.32755
NM_031380 // Fstl3 // follistatin-like 3 // 10 C1|10 // 83554 /// ENSMUST00000020575 //	Fstl3	4.24E-05	-2.32891
NM_001080769 // Uhrf1bp1 // UHRF1 (ICBP90) binding protein 1 // 17 A3.3|17 // 224648 //	Uhrf1bp1	0.000564468	-2.32991
NM_008990 // Pvrl2 // poliovirus receptor-related 2 // 7 A3|7 9.94 cM // 19294 /// ENSM	Pvrl2	0.000100864	-2.33091
---		6.07E-06	-2.33108
---		6.07E-06	-2.33108
NM_001284397 // Gngt2 // guanine nucleotide binding protein (G protein), gamma transduc	Gngt2	0.000380636	-2.33131
NM_172393 // Aim1 // absent in melanoma 1 // 10 B2|10 23.14 cM // 11630 /// ENSMUST0000	Aim1	7.56E-06	-2.3316
NM_001256515 // AI837181 // expressed sequence AI837181 // 19 A|19 // 107242 /// NM_134	AI837181	9.76E-05	-2.33338
NM_145122 // Pex16 // peroxisomal biogenesis factor 16 // 2 E1|2 // 18633 /// ENSMUST00	Pex16	2.88E-05	-2.33617
---		0.00227385	-2.33844
XM_006530302 // Trafd1 // TRAF type zinc finger domain containing 1 // 5 F|5 // 231712	Trafd1	7.14E-08	-2.33876
NR_045324 // Gm19705 // predicted gene, 19705 // 1 E4-F|1 59.94 cM // 100503460 /// NR_	Gm19705	0.0027215	-2.3415
NM_145619 // Parp3 // poly (ADP-ribose) polymerase family, member 3 // 9 F1|9 // 235587	Parp3	1.12E-05	-2.34674
NM_023526 // Nkiras1 // NFKB inhibitor interacting Ras-like protein 1 // 14|14 A3 // 69	Nkiras1	0.000823428	-2.35021
NM_013885 // Clic4 // chloride intracellular channel 4 (mitochondrial) // 4 D3|4 // 298	Clic4	0.000432639	-2.35524
NM_009448 // Tuba1c // tubulin, alpha 1C // 15 F1|15 // 22146 /// ENSMUST00000058914 //	Tuba1c	7.31E-05	-2.35604
ENSMUST00000139214 // 4930430E12Rik // RIKEN cDNA 4930430E12 gene // --- // --- /// ENS	4930430E12Rik	3.78E-06	-2.3561
NM_009716 // Atf4 // activating transcription factor 4 // 15 E1|15 37.85 cM // 11911 //	Atf4	4.66E-06	-2.35746
NM_001110824 // Foxp4 // forkhead box P4 // 17 C|17 // 74123 /// NM_001110825 // Foxp4	Foxp4	0.00192242	-2.36225
---		0.00322059	-2.36295
NM_001122680 // Pvrl4 // poliovirus receptor-related 4 // 1 H2|1 // 71740 /// NM_027893	Pvrl4	0.000167128	-2.36392
ENSMUST00000032429 // Med21 // mediator complex subunit 21 // 6 G3|6 77.7 cM // 108098	Med21	0.000133525	-2.36463
NM_001113374 // Mocs2 // molybdenum cofactor synthesis 2 // 13 D2.2|13 // 17434 /// NM_	Mocs2	7.01E-05	-2.36557
NM_011109 // Pla2g2d // phospholipase A2, group IID // 4 D3|4 70.57 cM // 18782 /// ENS	Pla2g2d	0.00447822	-2.36783
NM_173027 // Ip6k3 // inositol hexaphosphate kinase 3 // 17 A3.3|17 // 271424 /// ENSMU	Ip6k3	0.00439446	-2.3707
NM_001039530 // Parp14 // poly (ADP-ribose) polymerase family, member 14 // 16 B3|16 //	Parp14	0.00127358	-2.37282
XM_006530858 // Inpp4b // inositol polyphosphate-4-phosphatase, type II // 8 C2|8 39.02	Inpp4b	0.00110877	-2.37819
NM_008670 // Naip1 // NLR family, apoptosis inhibitory protein 1 // 13 D1-D3|13 53.18 c	Naip1	2.03E-06	-2.38165
ENSMUST00000068569 // Bcl2a1b // B cell leukemia/lymphoma 2 related protein A1b // 9 E3	Bcl2a1b	0.000623851	-2.38324
NM_013654 // Ccl7 // chemokine (C-C motif) ligand 7 // 11 C|11 49.83 cM // 20306 /// EN	Ccl7	0.00150352	-2.38744
NM_010871 // Naip6 // NLR family, apoptosis inhibitory protein 6 // 13 D1|13 53.09 cM /	Naip6	0.000525516	-2.3904
NM_178728 // Napepld // N-acyl phosphatidylethanolamine phospholipase D // 5 A3|5 // 24	Napepld	0.000247041	-2.39101
NM_023655 // Trim29 // tripartite motif-containing 29 // 9 A5.1|9 // 72169 /// ENSMUST0	Trim29	0.00326675	-2.39199
NM_001142642 // Fbrsl1 // fibrosin-like 1 // 5 F|5 // 381668 /// NM_028596 // Fbrsl1 //	Fbrsl1	6.69E-05	-2.39265
NM_144559 // Fcgr4 // Fc receptor, IgG, low affinity IV // 1 H3|1 78.53 cM // 246256 //	Fcgr4	1.64E-06	-2.39319
NM_001164071 // Tank // TRAF family member-associated Nf-kappa B activator // 2 C1.3|2	Tank	3.66E-05	-2.39378

NR_040374 // A230028O05Rik // RIKEN cDNA A230028O05 gene // 16 B1|16 // 319487 /// ENSM	A230028O05Rik	0.000109621	-2.39503
ENSMUST00000136542 // Gm11772 // predicted gene 11772 // --- // ---	Gm11772	0.0045589	-2.39584
ENSMUST00000160432 // Gm16231 // predicted gene 16231 // --- // ---	Gm16231	0.000313293	-2.39589
NM_001141981 // Rbm43 // RNA binding motif protein 43 // 2|2 C1 // 71684 /// NM_0011419	Rbm43	1.34E-06	-2.40032
NM_025730 // Lrrk2 // leucine-rich repeat kinase 2 // 15|15 F1 // 66725 /// XM_00652127	Lrrk2	6.74E-05	-2.40049
NM_007801 // Ctsh // cathepsin H // 9 E3.1|9 47.4 cM // 13036 /// ENSMUST00000034915 //	Ctsh	1.80E-05	-2.4011
NM_010628 // Kif9 // kinesin family member 9 // 9 F2|9 // 16578 /// XM_006511941 // Kif	Kif9	0.000536368	-2.40227
NM_029077 // Trim14 // tripartite motif-containing 14 // 4|4 B2 // 74735 /// ENSMUST000	Trim14	5.92E-06	-2.41186
NM_001048207 // Gypc // glycophorin C // 18 B1|18 18.05 cM // 71683 /// ENSMUST00000174	Gypc	8.15E-05	-2.41439
NM_001033136 // Rmdn3 // regulator of microtubule dynamics 3 // 2 E5|2 // 67809 /// ENS	Rmdn3	3.90E-05	-2.41515
NM_001038998 // Ccdc23 // coiled-coil domain containing 23 // 4 D2.1|4 // 69216 /// ENS	Ccdc23	0.000170594	-2.41629
ENSMUST00000101477 // Peli1 // pellino 1 // 11 A3.2|11 13.81 cM // 67245 /// AF302503 /	Peli1	4.91E-05	-2.41807
NM_001163590 // Stx11 // syntaxin 11 // 10 A1|10 // 74732 /// NM_029075 // Stx11 // syn	Stx11	0.00121746	-2.42205
NM_172722 // Naa25 // N(alpha)-acetyltransferase 25, NatB auxiliary subunit // 5 F|5 //	Naa25	6.32E-07	-2.42505
NM_016873 // Wisp2 // WNT1 inducible signaling pathway protein 2 // 2 H3|2 // 22403 ///	Wisp2	0.00245095	-2.42598
NM_001048060 // Idnk // idnK gluconokinase homolog (E. coli) // 13 B1|13 // 75731 /// N	Idnk	8.60E-05	-2.42637
ENSMUST00000164181 // Gm8894 // myosin light polypeptide 6 alkali smooth muscle and non	Gm8894	0.00337687	-2.42934
XR_140681 // 4930455G09Rik // RIKEN cDNA 4930455G09 gene // 4|4 // 78917 /// ENSMUST000	4930455G09Rik	0.000102308	-2.4294
---		0.00074689	-2.43102
NM_007498 // Atf3 // activating transcription factor 3 // 1 H6|1 96.28 cM // 11910 ///	Atf3	1.59E-07	-2.43244
NM_001025427 // Hmga1 // high mobility group AT-hook 1 // 17 A3.3|17 14.5 cM // 15361 /	Hmga1	6.47E-06	-2.43484
NM_008353 // Il12rb1 // interleukin 12 receptor, beta 1 // 8 B3.3|8 34.21 cM // 16161 /	Il12rb1	9.30E-05	-2.43677
NM_001160181 // Tor1aip2 // torsin A interacting protein 2 // 1 G3|1 // 240832 /// NM_0	Tor1aip2	3.47E-05	-2.44072
NM_019564 // Htra1 // HtrA serine peptidase 1 // 7 F3|7 // 56213 /// ENSMUST00000006367	Htra1	0.000142207	-2.44143
NM_172734 // Stk38l // serine/threonine kinase 38 like // 6 G3|6 // 232533 /// XM_00650	Stk38l	0.000277625	-2.44313
NM_010050 // Dio2 // deiodinase, iodothyronine, type II // 12 D3|12 // 13371 /// ENSMUS	Dio2	0.000421833	-2.45278
NM_172488 // Lacc1 // laccase (multicopper oxidoreductase) domain containing 1 // 14 D3	Lacc1	0.00333518	-2.45313
NM_008871 // Serpine1 // serine (or cysteine) peptidase inhibitor, clade E, member 1 //	Serpine1	0.000167515	-2.45348
NM_011030 // P4ha1 // procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydr	P4ha1	5.18E-06	-2.46161
NM_173052 // Serpinb1b // serine (or cysteine) peptidase inhibitor, clade B, member 1b	Serpinb1b	0.00276314	-2.46649
ENSMUST00000031670 // Gng11 // guanine nucleotide binding protein (G protein), gamma 11	Gng11	0.000347535	-2.46879
NM_001165919 // 1700123I01Rik // RIKEN cDNA 1700123I01 gene // 19 A|19 // 622554 /// XM	1700123I01Rik	6.23E-05	-2.47392
ENSMUST00000033900 // Rab20 // RAB20, member RAS oncogene family // 8 A1.1|8 5.73 cM //	Rab20	5.53E-05	-2.4746
XM_006543313 // 1700066C05Rik // RIKEN cDNA 1700066C05 gene // 16 C3.3|16 // 78654 ///	1700066C05Rik	0.00472468	-2.48008
NM_011426 // Siglec1 // sialic acid binding Ig-like lectin 1, sialoadhesin // 2 F-H1|2	Siglec1	2.68E-05	-2.48428
---		0.00491607	-2.48575
ENSMUST00000111314 // Adamts4 // a disintegrin-like and metallopeptidase (reprolysin ty	Adamts4	0.00504282	-2.48956
NM_001146348 // Eng // endoglin // 2 B|2 22.09 cM // 13805 /// NM_001146350 // Eng // e	Eng	8.79E-06	-2.49369
ENSMUST00000161540 // Gm17017 // predicted gene 17017 // --- // ---	Gm17017	4.18E-05	-2.49573
---		3.06E-05	-2.4961
NM_133661 // Slc6a12 // solute carrier family 6 (neurotransmitter transporter, betaine/	Slc6a12	0.000328268	-2.49863
NM_010734 // Lst1 // leukocyte specific transcript 1 // 17 B1|17 18.59 cM // 16988 ///	Lst1	0.00118117	-2.5037
NM_026929 // Chac1 // ChaC, cation transport regulator 1 // 2 E5|2 // 69065 /// ENSMUST	Chac1	0.00347382	-2.50389
NM_010548 // Il10 // interleukin 10 // 1 E4|1 56.89 cM // 16153 /// ENSMUST00000016673	Il10	0.00137487	-2.506
NM_207244 // Cd200r4 // CD200 receptor 4 // 16 B4|16 // 239849 /// XM_006522128 // Cd20	Cd200r4	6.51E-07	-2.50708
NM_027514 // Pvr // poliovirus receptor // 7 A3|7 9.95 cM // 52118 /// ENSMUST000000435	Pvr	0.000102952	-2.51035
NM_172668 // Lrp4 // low density lipoprotein receptor-related protein 4 // 2 E1|2 50.63	Lrp4	0.000260267	-2.51338
NM_001146308 // Dbnl // drebrin-like // 11 A1|11 3.87 cM // 13169 /// NM_001146309 // D	Dbnl	6.01E-06	-2.51397
NM_010757 // Mafk // v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (	Mafk	3.90E-06	-2.51404
NM_031178 // Tlr9 // toll-like receptor 9 // 9 F1|9 // 81897 /// ENSMUST00000062241 //	Tlr9	5.89E-05	-2.51771
NM_011163 // Eif2ak2 // eukaryotic translation initiation factor 2-alpha kinase 2 // 17	Eif2ak2	0.000509736	-2.52296
ENSMUST00000154924 // Pnpt1 // polyribonucleotide nucleotidyltransferase 1 // 11|11 A4	Pnpt1	3.28E-06	-2.52306
AK079938 // BE692007 // expressed sequence BE692007 // 19|19 8.44 cM // 100504727 /// X	BE692007	0.00358327	-2.52549
NM_009642 // Agtrap // angiotensin II, type I receptor-associated protein // 4 E1|4 78.	Agtrap	4.59E-06	-2.5258
NM_001177730 // Nr1h3 // nuclear receptor subfamily 1, group H, member 3 // 2 E1|2 50.5	Nr1h3	6.78E-06	-2.53437
---		0.00532235	-2.53608
ENSMUST00000174525 // H2-Q10 // histocompatibility 2, Q region locus 10 // 17 B1|17 18.	H2-Q10	0.00114793	-2.54313
NM_172697 // Prpf38a // PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	Prpf38a	1.90E-05	-2.5442
NM_001167991 // Hook2 // hook homolog 2 (Drosophila) // 8 C3|8 // 170833 /// NM_133255	Hook2	0.000680921	-2.54643
---		0.000399475	-2.55054
NM_053267 // Selm // selenoprotein M // 11 A1|11 // 114679 /// ENSMUST00000094469 // Se	Selm	1.66E-05	-2.55707
NM_145857 // Nod2 // nucleotide-binding oligomerization domain containing 2 // 8 C3|8 /	Nod2	0.000137645	-2.55843
NM_139128 // Coro6 // coronin 6 // 11 B5|11 // 216961 /// NM_139129 // Coro6 // coronin	Coro6	0.000418072	-2.57213
NM_007555 // Bmp5 // bone morphogenetic protein 5 // 9 D|9 42.34 cM // 12160 /// ENSMUS	Bmp5	0.000459215	-2.57515
ENSMUST00000025904 // Prdx5 // peroxiredoxin 5 // 19 A|19 5.08 cM // 54683 /// ENSMUST0	Prdx5	2.30E-06	-2.57932
AK037717 // A130040M12Rik // RIKEN cDNA A130040M12 gene // 11 C|11 // 319269	A130040M12Rik	0.000857389	-2.58326
NM_011756 // Zfp36 // zinc finger protein 36 // 7 A3|7 16.72 cM // 22695 /// ENSMUST000	Zfp36	4.46E-05	-2.58413
ENSMUST00000181222 // Gm16754 // predicted gene, 16754 // 9|9 7.74 cM // 100503569 ///	Gm16754	0.000866289	-2.58519
NM_001159301 // Lgals9 // lectin, galactose binding, soluble 9 // 11 B5|11 // 16859 ///	Lgals9	0.000197965	-2.58606
NM_001159393 // Irf1 // interferon regulatory factor 1 // 11 B1.3|11 32.0 cM // 16362 /	Irf1	0.00167596	-2.58738
NR_040442 // AV051173 // expressed sequence AV051173 // 4|4 // 100502959	AV051173	8.27E-05	-2.58751
NR_073559 // Stxbp3b // syntaxin-binding protein 3B // 19 A|19 // 619371 /// ENSMUST000	Stxbp3b	0.00518755	-2.592
NM_001252459 // Cyfip2 // cytoplasmic FMR1 interacting protein 2 // 11|11 B1.2 // 76884	Cyfip2	2.03E-07	-2.59335
NM_001110305 // Keap1 // kelch-like ECH-associated protein 1 // 9 A3|9 // 50868 /// NM_	Keap1	6.99E-05	-2.59816
ENSMUST00000073080 // Cycs // cytochrome c, somatic // 6 B2.3|6 24.32 cM // 13063	Cycs	0.000156804	-2.60145
NR_028589 // Gm14005 // predicted gene 14005 // 2 F1|2 // 100043424 /// NR_028590 // Gm	Gm14005	0.00138646	-2.60181
NR_045932 // Slfn5os // schlafen 5, opposite strand // 11 C|11 // 76392 /// ENSMUST0000	Slfn5os	4.02E-05	-2.60185
XR_392965 // 1110002J07Rik // RIKEN cDNA 1110002J07 gene // 10|10 // 68488 /// ENSMUST0	1110002J07Rik	0.00334135	-2.60518
NM_207105 // H2-Ab1 // histocompatibility 2, class II antigen A, beta 1 // 17 B1|17 17.	H2-Ab1	0.000117317	-2.60702
NM_011504 // Stxbp3a // syntaxin binding protein 3A // 3 F3|3 // 20912 /// ENSMUST00000	Stxbp3a	2.82E-05	-2.61196
NM_011189 // Psme1 // proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	Psme1	3.33E-06	-2.61561
ENSMUST00000181212 // 2310031A07Rik // RIKEN cDNA 2310031A07 gene // --- // --- /// AK0	2310031A07Rik	0.00309526	-2.62066
XM_006533512 // Slc22a4 // solute carrier family 22 (organic cation transporter), membe	Slc22a4	4.83E-06	-2.63049
ENSMUST00000172796 // Gm20496 // predicted gene 20496 // --- // --- /// ENSMUST00000173	Gm20496	0.00340254	-2.63631
NM_010637 // Klf4 // Kruppel-like factor 4 (gut) // 4 B3|4 29.76 cM // 16600 /// ENSMUS	Klf4	0.000811499	-2.63856
XM_006543523 // Gm7160 // predicted gene 7160 // 1 E2.1|1 // 635504	Gm7160	0.000459108	-2.63966
XM_006544796 // Gm10499 // predicted gene 10499 // 17 B1|17 // 69717 /// ENSMUST0000017	Gm10499	0.000949221	-2.64043
NM_007611 // Casp7 // caspase 7 // 19 D2|19 51.84 cM // 12369 /// ENSMUST00000026062 //	Casp7	0.000606381	-2.64162
NM_007523 // Bak1 // BCL2-antagonist/killer 1 // 17|17 B // 12018 /// ENSMUST0000002503	Bak1	2.41E-05	-2.6424

NM_009890 // Ch25h // cholesterol 25-hydroxylase // 19 C1|19 // 12642 /// ENSMUST000000	Ch25h	0.00264177	-2.64594
NM_001097980 // Gm16390 // predicted gene 16390 // X F3|X // 100040937 /// ENSMUST00000	Gm16390	0.00422242	-2.64628
NM_174850 // Micall2 // MICAL-like 2 // 5 G2|5 // 231830 /// ENSMUST00000044642 // Mica	Micall2	0.00146832	-2.64674
NM_030743 // Rnf114 // ring finger protein 114 // 2 H3|2 // 81018 /// XM_006500439 // R	Rnf114	1.16E-06	-2.64689
NM_008416 // Junb // jun B proto-oncogene // 8 C2-D1|8 41.41 cM // 16477 /// ENSMUST000	Junb	4.18E-08	-2.65596
NM_001033290 // Gpr55 // G protein-coupled receptor 55 // 1 C5|1 // 227326 /// XM_00652	Gpr55	1.74E-05	-2.66508
ENSMUST00000109212 // Gm5431 // predicted gene 5431 // 11 B1.2|11 // 432555	Gm5431	0.000554103	-2.66563
NM_001128605 // Psen2 // presenilin 2 // 1 H4|1 84.19 cM // 19165 /// NM_011183 // Psen	Psen2	1.35E-05	-2.66847
NM_001048177 // Jak2 // Janus kinase 2 // 19 C1|19 23.73 cM // 16452 /// NM_008413 // J	Jak2	0.00206559	-2.67129
NM_001126182 // Naip2 // NLR family, apoptosis inhibitory protein 2 // 13 D1|13 53.01 c	Naip2	0.000257077	-2.67431
NM_025821 // Carhsp1 // calcium regulated heat stable protein 1 // 16 A1|16 4.26 cM //	Carhsp1	4.49E-05	-2.67486
XM_006504642 // Gm15753 // predicted gene 15753 // 5 G2|5 // 624083	Gm15753	0.000626721	-2.6835
---		0.00305952	-2.69175
---		0.00305952	-2.69175
NM_008748 // Dusp8 // dual specificity phosphatase 8 // 7 F5|7 87.59 cM // 18218 /// EN	Dusp8	0.000971951	-2.69888
NM_012044 // Pla2g2e // phospholipase A2, group IIE // 4 D3|4 // 26970 /// ENSMUST00000	Pla2g2e	9.90E-05	-2.70094
NR_030490 // Mir709 // microRNA 709 // 8|8 // 735271 /// ENSMUST00000102190 // Mir709 /	Mir709	0.000483095	-2.70321
NM_026827 // Tmem219 // transmembrane protein 219 // 7|7 F4 // 68742 /// NM_028389 // T	Tmem219	2.21E-05	-2.70515
NM_001033310 // Cox18 // cytochrome c oxidase assembly protein 18 // 5 E1|5 // 231430 /	Cox18	3.49E-06	-2.70979
NM_133871 // Ifi44 // interferon-induced protein 44 // 3 H3|3 // 99899 /// ENSMUST00000	Ifi44	0.000188361	-2.71458
ENSMUST00000173249 // Gm20412 // predicted gene 20412 // --- // ---	Gm20412	1.38E-05	-2.7172
ENSMUST00000031766 // Asns // asparagine synthetase // 6 A1|6 // 27053 /// NM_012055 //	Asns	4.66E-07	-2.71837
NR_045641 // F630111L10Rik // RIKEN cDNA F630111L10 gene // 3 D|3 // 320463 /// AK17084	F630111L10Rik	1.05E-05	-2.71976
ENSMUST00000119109 // Etv3 // ets variant 3 // 3 F1|3 // 27049 /// NM_001083318 // Etv3	Etv3	1.16E-06	-2.72481
ENSMUST00000157098 // Gm26278 // predicted gene, 26278 // --- // ---	Gm26278	0.00113827	-2.72966
NM_011785 // Akt3 // thymoma viral proto-oncogene 3 // 1|1 H4-H6 // 23797 /// XM_006496	Akt3	3.52E-06	-2.73105
NM_173051 // Serpinb1c // serine (or cysteine) peptidase inhibitor, clade B, member 1c	Serpinb1c	0.000144642	-2.74145
NM_018825 // Sh2b2 // SH2B adaptor protein 2 // 5|5 G1 // 23921 /// XM_006504420 // Sh2	Sh2b2	7.17E-05	-2.74343
NM_029084 // Slamf8 // SLAM family member 8 // 1|1 H2 // 74748 /// ENSMUST00000065679 /	Slamf8	0.00035631	-2.74359
NM_026115 // Hat1 // histone aminotransferase 1 // 2 C2|2 // 107435 /// ENSMUST00000028	Hat1	5.22E-06	-2.74458
NM_021547 // Stard3 // START domain containing 3 // 11 D|11 // 59045 /// XM_006533897 /	Stard3	7.84E-07	-2.74928
NM_001009573 // Unc13d // unc-13 homolog D (C. elegans) // 11 E2|11 // 70450 /// ENSMUS	Unc13d	5.82E-06	-2.75205
NM_011957 // Creb3l1 // cAMP responsive element binding protein 3-like 1 // 2 E1|2 // 2	Creb3l1	0.000214894	-2.76329
NM_013819 // H2-M3 // histocompatibility 2, M region locus 3 // 17 B1|17 19.16 cM // 14	H2-M3	6.23E-07	-2.7666
XR_397421 // Gm19412 // predicted gene, 19412 // 17|17 17.98 cM // 100502849	Gm19412	1.44E-05	-2.76737
NM_001130476 // Tpst1 // protein-tyrosine sulfotransferase 1 // 5|5 F-G1 // 22021 /// N	Tpst1	0.000629664	-2.77363
---		3.32E-06	-2.78168
ENSMUST00000104261 // Gm23127 // predicted gene, 23127 // --- // --- /// AK163470 // El	Gm23127	0.000194416	-2.78272
NM_013640 // Psmb10 // proteasome (prosome, macropain) subunit, beta type 10 // 8 D3|8	Psmb10	0.000211328	-2.79112
NM_021272 // Fabp7 // fatty acid binding protein 7, brain // 10 B4|10 // 12140 /// ENSM	Fabp7	5.76E-07	-2.79452
NM_029219 // Rnf19b // ring finger protein 19B // 4|4 D2.3 // 75234 /// ENSMUST00000030	Rnf19b	1.98E-06	-2.79552
NM_026840 // Pdgfrl // platelet-derived growth factor receptor-like // 8 A4|8 // 68797	Pdgfrl	1.64E-05	-2.79586
ENSMUST00000160076 // Gm16213 // predicted gene 16213 // --- // ---	Gm16213	0.00193404	-2.80082
NM_001101467 // Cyp2a22 // cytochrome P450, family 2, subfamily a, polypeptide 22 // 7	Cyp2a22	0.00403914	-2.80326
NM_001170853 // Mndal // myeloid nuclear differentiation antigen like // 1 H3|1 // 1000	Mndal	0.000649485	-2.80361
NM_001167946 // Zfp821 // zinc finger protein 821 // 8 D3|8 // 75871 /// NM_001286391 /	Zfp821	3.59E-05	-2.81239
NM_001146318 // Cnp // 2,3-cyclic nucleotide 3 phosphodiesterase // 11 D|11 63.47 cM //	Cnp	1.97E-05	-2.81779
NM_001161847 // Sgk1 // serum/glucocorticoid regulated kinase 1 // 10 A3|10 // 20393 //	Sgk1	7.62E-08	-2.81889
NM_001029929 // Zmynd15 // zinc finger, MYND-type containing 15 // 11 B3|11 // 574428 /	Zmynd15	6.04E-07	-2.82019
NM_001081020 // Adamts6 // a disintegrin-like and metallopeptidase (reprolysin type) wi	Adamts6	7.65E-05	-2.83431
NM_016767 // Batf // basic leucine zipper transcription factor, ATF-like // 12 D2|12 //	Batf	0.000315305	-2.84022
NM_183201 // Slfn5 // schlafen 5 // 11 C|11 // 327978 /// XR_388481 // Slfn5 // schlafe	Slfn5	4.57E-05	-2.84258
NM_015811 // Rgs1 // regulator of G-protein signaling 1 // 1 F|1 62.56 cM // 50778 ///	Rgs1	2.56E-05	-2.85173
NM_008654 // Ppp1r15a // protein phosphatase 1, regulatory (inhibitor) subunit 15A // 7	Ppp1r15a	6.29E-06	-2.85307
NM_001163573 // Scnm1 // sodium channel modifier 1 // 3 F2|3 40.74 cM // 69269 /// NM_0	Scnm1	2.05E-05	-2.85328
NM_011066 // Per2 // period circadian clock 2 // 1|1 C5 // 18627 /// ENSMUST00000069620	Per2	1.66E-05	-2.87106
NM_001162365 // Ptk2b // PTK2 protein tyrosine kinase 2 beta // 14 D1|14 34.36 cM // 19	Ptk2b	3.72E-07	-2.88217
ENSMUST00000032815 // Nfkbib // nuclear factor of kappa light polypeptide gene enhancer	Nfkbib	9.28E-05	-2.88393
ENSMUST00000049281 // Fam53c // family with sequence similarity 53, member C // 18 B1|1	Fam53c	8.45E-05	-2.89129
NM_026942 // Stoml1 // stomatin-like 1 // 9 B|9 // 69106 /// NR_028146 // Stoml1 // sto	Stoml1	0.00028948	-2.8958
NM_001166537 // Hmga1 // high mobility group AT-hook 1 // 17 A3.3|17 14.5 cM // 15361 /	Hmga1	8.29E-05	-2.90804
ENSMUST00000168579 // Slc16a3 // solute carrier family 16 (monocarboxylic acid transpor	Slc16a3	8.58E-07	-2.91824
NM_021430 // Rilpl1 // Rab interacting lysosomal protein-like 1 // 5|5 F // 75695 /// X	Rilpl1	6.44E-07	-2.91906
NM_019580 // Gde1 // glycerophosphodiester phosphodiesterase 1 // 7|7 F3 // 56209 /// E	Gde1	2.42E-06	-2.9229
NM_198861 // Lrrc75a // leucine rich repeat containing 75A // 11 B2|11 // 192976 /// XM	Lrrc75a	7.66E-07	-2.92437
NM_172728 // Creb5 // cAMP responsive element binding protein 5 // 6 B3|6 25.9 cM // 23	Creb5	1.35E-05	-2.92737
NM_001287738 // Cebpb // CCAAT/enhancer binding protein (C/EBP), beta // 2 H3|2 87.58 c	Cebpb	7.62E-06	-2.93332
NM_001271760 // Adra1a // adrenergic receptor, alpha 1a // 14 D1|14 // 11549 /// NM_001	Adra1a	3.06E-06	-2.93516
ENSMUST00000157375 // Gm25493 // predicted gene, 25493 // --- // ---	Gm25493	0.000933322	-2.94095
NM_080555 // Ppap2b // phosphatidic acid phosphatase type 2B // 4 C6|4 49.18 cM // 6791	Ppap2b	4.36E-06	-2.94101
NM_001163833 // Msl3l2 // male-specific lethal 3-like 2 (Drosophila) // 10 B3|10 // 733	Msl3l2	0.000138415	-2.94158
NM_009878 // Cdkn2d // cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) // 9 A	Cdkn2d	2.10E-05	-2.94579
---		4.35E-06	-2.94856
NM_028287 // Zufsp // zinc finger with UFM1-specific peptidase domain // 10 B1|10 // 72	Zufsp	7.86E-07	-2.94927
ENSMUST00000122776 // Gm24141 // predicted gene, 24141 // --- // ---	Gm24141	0.00327246	-2.95377
NM_025541 // Asf1a // anti-silencing function 1A histone chaperone // 10 B3|10 // 66403	Asf1a	4.88E-06	-2.95638
NR_015514 // 9330175E14Rik // RIKEN cDNA 9330175E14 gene // 8 C5|8 // 320377 /// ENSMUS	9330175E14Rik	0.00124518	-2.95989
NM_197944 // Hsh2d // hematopoietic SH2 domain containing // 8 B3.3|8 // 209488 /// ENS	Hsh2d	6.50E-05	-2.97916
ENSMUST00000097355 // 4930403O15Rik // RIKEN cDNA 4930403O15 gene // --- // --- /// AK0	4930403O15Rik	0.00234396	-2.9863
NM_172839 // Ccnj // cyclin J // 19 C3|19 // 240665 /// ENSMUST00000025983 // Ccnj // c	Ccnj	2.74E-05	-2.98786
---		0.00019928	-2.98883
NM_172833 // Malt1 // mucosa associated lymphoid tissue lymphoma translocation gene 1 /	Malt1	0.00450255	-2.99553
NM_031373 // Ogfr // opioid growth factor receptor // 2 H4|2 // 72075 /// ENSMUST000000	Ogfr	3.93E-07	-3.02452
NM_153760 // Mill2 // MHC I like leukocyte 2 // 7 A3|7 9.35 cM // 243864 /// NM_153761	Mill2	0.00064121	-3.02524
NM_029508 // Pcgf5 // polycomb group ring finger 5 // 19 C2|19 // 76073 /// XM_00652743	Pcgf5	0.000296584	-3.03928
NM_010333 // S1pr2 // sphingosine-1-phosphate receptor 2 // 9 A3|9 7.68 cM // 14739 ///	S1pr2	3.12E-07	-3.04962
NM_008967 // Ptgir // prostaglandin I receptor (IP) // 7 A2|7 9.15 cM // 19222 /// XM_0	Ptgir	1.48E-05	-3.05037
NM_001290413 // Traf2 // TNF receptor-associated factor 2 // 2 A3|2 // 22030 /// NM_009	Traf2	3.33E-06	-3.06503
NM_178890 // Abtb2 // ankyrin repeat and BTB (POZ) domain containing 2 // 2 E2|2 // 993	Abtb2	3.18E-06	-3.06555

NM_013671 // Sod2 // superoxide dismutase 2, mitochondrial // 17 A1|17 8.75 cM // 20656	Sod2	0.00107675	-3.07239
AK089726 // Trim30a // tripartite motif-containing 30A // 7 E3|7 55.69 cM // 20128	Trim30a	0.00200827	-3.07333
ENSMUST00000168990 // Gm17034 // predicted gene 17034 // --- // ---	Gm17034	0.00490031	-3.08109
NM_011333 // Ccl2 // chemokine (C-C motif) ligand 2 // 11 C-E1|11 49.82 cM // 20296 ///	Ccl2	0.00229801	-3.08236
NM_145458 // Pxk // PX domain containing serine/threonine kinase // 14 A1|14 4.7 cM //	Pxk	1.55E-08	-3.08854
NM_016972 // Slc7a8 // solute carrier family 7 (cationic amino acid transporter, y+ sys	Slc7a8	2.71E-08	-3.09091
XR_375897 // Gm12474 // predicted gene 12474 // 3 F2.2|3 // 545557 /// XR_375898 // Gm1	Gm12474	1.66E-05	-3.09646
---		0.000285409	-3.09826
---		0.00301504	-3.09923
---		0.000233126	-3.10483
NM_010156 // Samd9l // sterile alpha motif domain containing 9-like // 6 A1-A2|6 1.76 c	Samd9l	3.60E-06	-3.10642
NM_145523 // Gca // grancalcin // 2 C1.3|2 // 227960 /// ENSMUST00000028257 // Gca // g	Gca	0.0008629	-3.11007
NM_001033245 // Hk3 // hexokinase 3 // 13 B1|13 // 212032 /// NM_001206390 // Hk3 // he	Hk3	3.04E-08	-3.11156
NM_026960 // Gsdmd // gasdermin D // 15|15 D3-E1 // 69146 /// XM_006521343 // Gsdmd //	Gsdmd	1.76E-06	-3.12406
NM_033541 // Oas1c // 2-5 oligoadenylate synthetase 1C // 5 F|5 60.64 cM // 114643 ///	Oas1c	2.62E-06	-3.12673
NM_172293 // Pced1b // PC-esterase domain containing 1B // 15 F1|15 // 239647 /// XM_00	Pced1b	0.000809355	-3.12891
NM_001040026 // Sco1 // SCO cytochrome oxidase deficient homolog 1 (yeast) // 11 B3|11	Sco1	1.09E-05	-3.13897
NM_001033308 // Themis2 // thymocyte selection associated family member 2 // 4 D2.3|4 /	Themis2	8.69E-08	-3.14662
XR_374962 // Gm14010 // predicted gene 14010 // 2 F1|2 // 100043729 /// ENSMUST00000131	Gm14010	0.00364976	-3.14741
NM_145391 // Tapbpl // TAP binding protein-like // 6 F3|6 // 213233 /// XM_006505862 //	Tapbpl	0.000276182	-3.14743
ENSMUST00000079684 // Gm8394 // predicted gene 8394 // --- // ---	Gm8394	1.00E-07	-3.1508
NM_010442 // Hmox1 // heme oxygenase (decycling) 1 // 8 C1|8 35.59 cM // 15368 /// ENSM	Hmox1	3.28E-07	-3.15669
NM_001033450 // Mnda // myeloid cell nuclear differentiation antigen // 1 H3|1 // 38130	Mnda	0.00165775	-3.15731
NM_001145979 // Gtpbp2 // GTP binding protein 2 // 17|17 C-D // 56055 /// NM_019581 //	Gtpbp2	4.93E-07	-3.16118
ENSMUST00000129913 // Igf2bp2 // insulin-like growth factor 2 mRNA binding protein 2 //	Igf2bp2	3.75E-06	-3.16564
NM_133955 // Rhou // ras homolog gene family, member U // 8 E2|8 // 69581 /// ENSMUST00	Rhou	0.000897679	-3.17878
XM_006533108 // Rhbdf2 // rhomboid 5 homolog 2 (Drosophila) // 11 E2|11 // 217344 /// E	Rhbdf2	3.12E-06	-3.18049
NM_001169131 // Papd7 // PAP associated domain containing 7 // 13 C1|13 35.55 cM // 210	Papd7	2.38E-05	-3.18327
NM_011414 // Slpi // secretory leukocyte peptidase inhibitor // 2 H|2 // 20568 /// ENSM	Slpi	0.000827033	-3.18369
ENSMUST00000139725 // Mitd1 // MIT, microtubule interacting and transport, domain conta	Mitd1	1.18E-05	-3.1859
NM_001172117 // Hck // hemopoietic cell kinase // 2 H1|2 75.41 cM // 15162 /// NM_01040	Hck	0.000102354	-3.18938
NM_010276 // Gem // GTP binding protein (gene overexpressed in skeletal muscle) // 4 A1	Gem	0.00212387	-3.19089
NM_183180 // Tspan18 // tetraspanin 18 // 2 E1|2 // 241556 /// XM_006499474 // Tspan18	Tspan18	0.002735	-3.19127
NM_001122675 // Zcchc2 // zinc finger, CCHC domain containing 2 // 1 E2.1|1 // 227449 /	Zcchc2	3.05E-05	-3.19161
NM_010049 // Dhfr // dihydrofolate reductase // 13 C3|13 47.64 cM // 13361 /// ENSMUST0	Dhfr	4.39E-05	-3.19688
NM_027411 // Spdl1 // spindle apparatus coiled-coil protein 1 // 11|11 A5 // 70385 ///	Spdl1	7.98E-06	-3.20789
NM_001081005 // 1500012F01Rik // RIKEN cDNA 1500012F01 gene // 2 H3|2 // 68949 /// ENSM	1500012F01Rik	1.80E-05	-3.21437
NM_008842 // Pim1 // proviral integration site 1 // 17 A3.3|17 15.38 cM // 18712 /// EN	Pim1	7.02E-05	-3.21791
NM_001008497 // P2ry14 // purinergic receptor P2Y, G-protein coupled, 14 // 3 D|3 28.96	P2ry14	1.70E-06	-3.22143
NM_134102 // Pla1a // phospholipase A1 member A // 16 B4|16 26.83 cM // 85031 /// XM_00	Pla1a	0.000877393	-3.22149
NM_010829 // Msh3 // mutS homolog 3 (E. coli) // 13 C3|13 47.63 cM // 17686 /// XM_0065	Msh3	3.22E-05	-3.2232
NM_001145827 // Stk40 // serine/threonine kinase 40 // 4 D2.2|4 // 74178 /// NM_028800	Stk40	3.50E-05	-3.22702
NM_001004185 // Whamm // WAS protein homolog associated with actin, golgi membranes and	Whamm	8.23E-07	-3.23432
NM_009763 // Bst1 // bone marrow stromal cell antigen 1 // 5 B3|5 23.84 cM // 12182 ///	Bst1	3.11E-07	-3.23445
NR_033498 // AI504432 // expressed sequence AI504432 // 3 F2.3|3 // 229694 /// ENSMUST0	AI504432	0.00317637	-3.23711
NM_009807 // Casp1 // caspase 1 // 9 A1|9 2.46 cM // 12362 /// ENSMUST00000027015 // Ca	Casp1	2.41E-05	-3.24466
NM_029809 // 2310014L17Rik // RIKEN cDNA 2310014L17 gene // 7 A1|7 // 381845 /// ENSMUS	2310014L17Rik	0.00314391	-3.24548
NM_001013371 // Dtx3l // deltex 3-like (Drosophila) // 16 B3|16 // 209200 /// ENSMUST00	Dtx3l	1.78E-06	-3.24748
NM_001083616 // Cacna1d // calcium channel, voltage-dependent, L type, alpha 1D subunit	Cacna1d	1.89E-05	-3.25373
NM_023386 // Rtp4 // receptor transporter protein 4 // 16 B1|16 // 67775 /// XM_0065224	Rtp4	9.94E-07	-3.25465
NM_008884 // Pml // promyelocytic leukemia // 9 B|9 31.63 cM // 18854 /// NM_178087 //	Pml	4.17E-06	-3.26757
NM_001038587 // Adar // adenosine deaminase, RNA-specific // 3|3 F2 // 56417 /// NM_001	Adar	5.77E-07	-3.26936
NM_001005423 // Mreg // melanoregulin // 1 C3|1 // 381269 /// XM_006496111 // Mreg // m	Mreg	0.000302846	-3.27663
---		0.00179902	-3.28184
---		0.00199535	-3.28477
NM_013673 // Sp100 // nuclear antigen Sp100 // 1 C5|1 43.6 cM // 20684 /// XM_006529287	Sp100	6.44E-06	-3.28498
NM_175648 // Trim30b // tripartite motif-containing 30B // 7 E3|7 // 244183 /// ENSMUST	Trim30b	0.000568544	-3.29327
---		0.00327647	-3.29799
---		0.00350455	-3.30007
NM_008360 // Il18 // interleukin 18 // 9 A5.3|9 27.75 cM // 16173 /// XM_006510023 // I	Il18	0.00016425	-3.30081
ENSMUST00000106283 // Rims3 // regulating synaptic membrane exocytosis 3 // 4 D2.2|4 //	Rims3	0.000342044	-3.30589
NM_007536 // Bcl2a1d // B cell leukemia/lymphoma 2 related protein A1d // 9 E3.1|9 // 1	Bcl2a1d	0.000370551	-3.30744
XM_006502252 // Rapgef2 // Rap guanine nucleotide exchange factor (GEF) 2 // 3 E3|3 //	Rapgef2	0.000747305	-3.32171
NR_045458 // 4933433H22Rik // RIKEN cDNA 4933433H22 gene // 17|17 // 74473	4933433H22Rik	0.000209913	-3.32766
NM_010496 // Id2 // inhibitor of DNA binding 2 // 12 B|12 8.57 cM // 15902 /// ENSMUST0	Id2	8.62E-09	-3.3295
ENSMUST00000111276 // Slamf7 // SLAM family member 7 // 1|1 H2 // 75345 /// AB196816 //	Slamf7	3.16E-05	-3.33385
NM_001045481 // Ifi203 // interferon activated gene 203 // 1 H3|1 80.76 cM // 15950 ///	Ifi203	2.01E-05	-3.33458
NM_017466 // Ccrl2 // chemokine (C-C motif) receptor-like 2 // 9 F|9 60.92 cM // 54199	Ccrl2	0.000580599	-3.34799
NM_008328 // Ifi203 // interferon activated gene 203 // 1 H3|1 80.76 cM // 15950 /// EN	Ifi203	8.12E-05	-3.35449
NM_175401 // Fbxw17 // F-box and WD-40 domain protein 17 // 13 A5|13 // 109082 /// XM_0	Fbxw17	1.31E-08	-3.35926
---		1.71E-05	-3.36288
ENSMUST00000102409 // Gm24049 // predicted gene, 24049 // --- // ---	Gm24049	0.00205167	-3.3647
NM_133217 // Bco2 // beta-carotene oxygenase 2 // 9|9 B // 170752 /// XM_006510045 // B	Bco2	0.0013708	-3.36828
NM_019915 // Art2b // ADP-ribosyltransferase 2b // 7 E3|7 54.61 cM // 11872 /// XM_0065	Art2b	0.00513279	-3.36856
NM_001081005 // 1500012F01Rik // RIKEN cDNA 1500012F01 gene // 2 H3|2 // 68949 /// ENSM	1500012F01Rik	1.35E-06	-3.40877
NM_008367 // Il2ra // interleukin 2 receptor, alpha chain // 2 A2-A3|2 8.91 cM // 16184	Il2ra	0.0010101	-3.42186
NM_175382 // Fam72a // family with sequence similarity 72, member A // 1 E4|1 // 108900	Fam72a	1.69E-05	-3.42598
NM_013673 // Sp100 // nuclear antigen Sp100 // 1 C5|1 43.6 cM // 20684 /// XM_006529287	Sp100	2.57E-05	-3.42811
NM_001252568 // Phyhd1 // phytanoyl-CoA dioxygenase domain containing 1 // 2 B|2 // 227	Phyhd1	7.25E-05	-3.4436
NM_001163489 // Sema4a // sema domain, immunoglobulin domain (Ig), transmembrane domain	Sema4a	3.19E-09	-3.44711
NM_001164566 // Spats2l // spermatogenesis associated, serine-rich 2-like // 1|1 C2 //	Spats2l	0.00347238	-3.44873
NM_001253817 // Tmem184b // transmembrane protein 184b // 15 E1|15 // 223693 /// NM_001	Tmem184b	1.70E-07	-3.45596
XM_006517419 // Slc6a19 // solute carrier family 6 (neurotransmitter transporter), memb	Slc6a19	0.000357784	-3.46428
---		2.85E-06	-3.46462
NM_025446 // Aig1 // androgen-induced 1 // 10 A2|10 // 66253 /// ENSMUST00000019942 //	Aig1	7.37E-06	-3.46555
NM_001168334 // Gm2799 // predicted gene 2799 // X A3.1|X // 100040482 /// ENSMUST00000	Gm2799	0.000161184	-3.47244
---		0.00245377	-3.47887
XM_006497078 // LOC102639543 // pyrin domain-containing protein 3-like // --- // 102639	LOC102639543	0.00173044	-3.48243
ENSMUST00000111360 // LOC100041057 // nuclear body protein SP140-like // 1|1 // 1000410	LOC100041057	0.00219959	-3.48316

NM_025659 // Abi3 // ABI gene family, member 3 // 11 D|11 // 66610 /// XM_006533953 //	Abi3	1.76E-06	-3.49087
NM_001198765 // Postn // periostin, osteoblast specific factor // 3 C|3 // 50706 /// NM	Postn	3.03E-05	-3.49613
ENSMUST00000029140 // Procr // protein C receptor, endothelial // 2|2 H1-3 // 19124 ///	Procr	5.03E-06	-3.50157
NM_010186 // Fcgr1 // Fc receptor, IgG, high affinity I // 3 F2.1|3 41.72 cM // 14129 /	Fcgr1	6.10E-07	-3.50343
NM_001111304 // Tbc1d9 // TBC1 domain family, member 9 // 8|8 C3 // 71310 /// NM_027758	Tbc1d9	8.36E-09	-3.5102
NM_023731 // Ccdc86 // coiled-coil domain containing 86 // 19 B|19 7.41 cM // 108673 //	Ccdc86	3.25E-05	-3.51466
NR_030251 // Mir483 // microRNA 483 // 7|7 // 723874 /// ENSMUST00000093631 // Mir483 /	Mir483	0.000803811	-3.52225
NR_030251 // Mir483 // microRNA 483 // 7|7 // 723874 /// ENSMUST00000093631 // Mir483 /	Mir483	0.000803811	-3.52225
XM_006497081 // Gm16340 // predicted gene 16340 // 1|1 80.65 cM // 100504287 /// ENSMUS	Gm16340	0.000231527	-3.52596
NM_181344 // C1rl // complement component 1, r subcomponent-like // 6 F2|6 // 232371 //	C1rl	9.36E-08	-3.52718
NM_001290475 // Tdrd7 // tudor domain containing 7 // 4 B1|4 // 100121 /// NM_146142 //	Tdrd7	8.69E-07	-3.52765
NM_145968 // Tagap // T cell activation Rho GTPase activating protein // 17 A1|17 // 72	Tagap	0.00043789	-3.5501
NM_172785 // Zc3h12d // zinc finger CCCH type containing 12D // 10 A1|10 // 237256 ///	Zc3h12d	4.11E-05	-3.58021
NM_001289568 // Sass6 // spindle assembly 6 homolog (C. elegans) // 3|3 G2 // 72776 ///	Sass6	0.000132573	-3.58829
NM_133954 // Usb1 // U6 snRNA biogenesis 1 // 8 D1|8 // 101985 /// ENSMUST00000034245 /	Usb1	1.59E-06	-3.60149
NM_133821 // Phlpp1 // PH domain and leucine rich repeat protein phosphatase 1 // 1 E2.	Phlpp1	4.81E-06	-3.61318
NM_011409 // Slfn3 // schlafen 3 // 11 C|11 // 20557 /// XM_006532656 // Slfn3 // schla	Slfn3	4.94E-05	-3.61601
---		0.000754005	-3.63036
NM_001004157 // Scarf1 // scavenger receptor class F, member 1 // 11 B5|11 // 380713 //	Scarf1	5.85E-05	-3.63821
NM_175236 // Adhfe1 // alcohol dehydrogenase, iron containing, 1 // 1 A2|1 // 76187 ///	Adhfe1	2.68E-05	-3.64459
NM_013875 // Pde7b // phosphodiesterase 7B // 10 A3|10 // 29863 /// XM_006512758 // Pde	Pde7b	5.02E-07	-3.69568
NM_013632 // Pnp // purine-nucleoside phosphorylase // 14 B-C1|14 26.31 cM // 18950 ///	Pnp	2.69E-05	-3.69956
NM_030253 // Parp9 // poly (ADP-ribose) polymerase family, member 9 // 16 B3|16 // 8028	Parp9	2.47E-06	-3.70141
NM_028019 // Rnf135 // ring finger protein 135 // 11 B5|11 47.59 cM // 71956 /// ENSMUS	Rnf135	3.60E-06	-3.70832
NM_008607 // Mmp13 // matrix metallopeptidase 13 // 9|9 A1-A2 // 17386 /// ENSMUST00000	Mmp13	0.00455139	-3.71477
NR_073523 // Slfn10-ps // schlafen 10, pseudogene // 11 C|11 // 237887 /// NR_073524 //	Slfn10-ps	5.51E-05	-3.72815
NM_001039562 // Ankrd37 // ankyrin repeat domain 37 // 8 B1.1|8 // 654824 /// ENSMUST00	Ankrd37	8.42E-05	-3.72951
XR_376538 // LOC102635290 // uncharacterized LOC102635290 // --- // 102635290 /// XR_37	LOC102635290	1.93E-06	-3.76778
NM_001204910 // AI607873 // expressed sequence AI607873 // 1 H3|1 // 226691 /// ENSMUST	AI607873	0.000280158	-3.78015
NM_001033632 // Ifitm6 // interferon induced transmembrane protein 6 // 7 F5|7 // 21300	Ifitm6	2.71E-05	-3.78413
NR_038025 // 4933412E12Rik // RIKEN cDNA 4933412E12 gene // 10|10 // 71086 /// NR_03802	4933412E12Rik	0.000588597	-3.79181
ENSMUST00000120177 // Gstt1 // glutathione S-transferase, theta 1 // 10 B5-C1|10 38.58	Gstt1	7.74E-06	-3.82939
---		9.35E-06	-3.8294
NM_177861 // Tmem67 // transmembrane protein 67 // 4 A1|4 // 329795 /// NR_110955 // Tm	Tmem67	1.00E-05	-3.83143
NM_026985 // Mcemp1 // mast cell expressed membrane protein 1 // 8 A1|8 1.92 cM // 6918	Mcemp1	0.000205747	-3.83643
NM_194346 // Rnf31 // ring finger protein 31 // 14 C3|14 // 268749 /// ENSMUST000000194	Rnf31	1.23E-06	-3.85626
NM_145373 // Sectm1a // secreted and transmembrane 1A // 11 E2|11 // 209588 /// XM_0065	Sectm1a	6.35E-06	-3.86014
NM_126166 // Tlr3 // toll-like receptor 3 // 8|8 B2 // 142980 /// XM_006509278 // Tlr3	Tlr3	3.45E-05	-3.86121
NM_009930 // Col3a1 // collagen, type III, alpha 1 // 1 C1.1|1 23.67 cM // 12825 /// EN	Col3a1	6.87E-05	-3.87022
NM_001161770 // Lmo4 // LIM domain only 4 // 3 H2|3 68.61 cM // 16911 /// ENSMUST000001	Lmo4	1.40E-06	-3.87171
NR_045146 // BC051226 // cDNA sequence BC051226 // 17 B1|17 // 407803 /// ENSMUST000001	BC051226	4.90E-06	-3.87747
ENSMUST00000160674 // Csprs // component of Sp100-rs // 8 B1.3|1 // 114564 /// ENSMUST0	Csprs	3.68E-05	-3.88243
NM_146064 // Soat2 // sterol O-acyltransferase 2 // 15 F3|15 57.33 cM // 223920 /// XM_	Soat2	0.000273837	-3.89195
NM_010724 // Psmb8 // proteasome (prosome, macropain) subunit, beta type 8 (large multi	Psmb8	3.26E-08	-3.89385
NM_001013616 // Trim6 // tripartite motif-containing 6 // 7 F1|7 55.55 cM // 94088 ///	Trim6	0.000118752	-3.91431
XR_390079 // LOC102634822 // uncharacterized LOC102634822 // --- // 102634822 /// XR_40	LOC102634822	0.000195999	-3.92183
NM_013558 // Hspa1l // heat shock protein 1-like // 17 B1|17 18.51 cM // 15482 /// ENSM	Hspa1l	0.00301875	-3.93412
NM_001002898 // Sirpb1a // signal-regulatory protein beta 1A // 3 A1|3 // 320832 /// EN	Sirpb1a	0.000197586	-3.93885
NM_001025246 // Trp53i11 // transformation related protein 53 inducible protein 11 // 2	Trp53i11	0.000334662	-3.95662
NM_007742 // Col1a1 // collagen, type I, alpha 1 // 11 D|11 59.01 cM // 12842 /// ENSMU	Col1a1	2.99E-06	-3.96343
ENSMUST00000103475 // Ighv14-4 // immunoglobulin heavy variable 14-4 // --- // --- ///	Ighv14-4	0.0021995	-3.97979
NM_139269 // Pla2g16 // phospholipase A2, group XVI // 19 A|19 // 225845 /// XM_0065269	Pla2g16	0.000290173	-3.98505
ENSMUST00000093902 // Rnf213 // ring finger protein 213 // 11 E2|11 83.48 cM // 672511	Rnf213	0.000260859	-4.01613
XM_006496589 // LOC101056250 // sp110 nuclear body protein-like // --- // 101056250 ///	LOC101056250	3.29E-05	-4.02587
NM_008206 // H2-Oa // histocompatibility 2, O region alpha locus // 17 B1|17 17.98 cM /	H2-Oa	0.00083914	-4.05266
NM_013825 // Ly75 // lymphocyte antigen 75 // 2 C1.1|2 // 17076 /// ENSMUST00000028362	Ly75	5.07E-06	-4.05775
NM_011530 // Tap2 // transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) // 17	Tap2	3.38E-08	-4.05894
NM_029472 // Gstt4 // glutathione S-transferase, theta 4 // 10 C1|10 // 75886 /// ENSMU	Gstt4	0.000234143	-4.06154
NM_010959 // Oit3 // oncoprotein induced transcript 3 // 10|10 B3 // 18302 /// ENSMUST0	Oit3	1.14E-07	-4.06408
NM_001012236 // Trex1 // three prime repair exonuclease 1 // 9 F2|9 // 22040 /// NM_011	Trex1	1.39E-05	-4.06789
NM_001035228 // St3gal5 // ST3 beta-galactoside alpha-2,3-sialyltransferase 5 // 6|6 C3	St3gal5	2.47E-07	-4.07571
NM_013822 // Jag1 // jagged 1 // 2 F3|2 67.73 cM // 16449 /// ENSMUST00000028735 // Jag	Jag1	6.02E-07	-4.082
NM_013754 // Insl6 // insulin-like 6 // 19|19 C3 // 27356 /// ENSMUST00000052380 // Ins	Insl6	5.98E-06	-4.08907
NM_145227 // Oas2 // 2-5 oligoadenylate synthetase 2 // 5 F|5 60.64 cM // 246728 /// XM	Oas2	5.00E-06	-4.09634
NM_011854 // Oasl2 // 2-5 oligoadenylate synthetase-like 2 // 5 F|5 // 23962 /// ENSMUS	Oasl2	1.19E-05	-4.10281
XM_006496589 // LOC101056250 // sp110 nuclear body protein-like // --- // 101056250 ///	LOC101056250	8.62E-05	-4.1096
---		0.00149029	-4.11467
NM_010484 // Slc6a4 // solute carrier family 6 (neurotransmitter transporter, serotonin	Slc6a4	2.66E-06	-4.12045
NM_021398 // Slc43a3 // solute carrier family 43, member 3 // 2 E1|2 // 58207 /// XM_00	Slc43a3	1.07E-06	-4.12147
NR_004446 // H2-K2 // histocompatibility 2, K region locus 2 // 17 B1|17 17.98 cM // 63	H2-K2	0.000328045	-4.12775
NM_008207 // H2-T24 // histocompatibility 2, T region locus 24 // 17 B1|17 18.84 cM //	H2-T24	7.86E-05	-4.12843
NM_022982 // Rtn4r // reticulon 4 receptor // 16 B1|16 // 65079 /// ENSMUST00000059589	Rtn4r	3.06E-06	-4.13618
NM_008608 // Mmp14 // matrix metallopeptidase 14 (membrane-inserted) // 14 C2|14 27.79	Mmp14	0.000434539	-4.15948
---		1.71E-05	-4.16551
XM_006544847 // LOC102642448 // schlafen family member 13-like // --- // 102642448 ///	LOC102642448	6.27E-06	-4.16646
NM_008216 // Has2 // hyaluronan synthase 2 // 15 D1|15 23.31 cM // 15117 /// ENSMUST000	Has2	2.16E-07	-4.17085
NR_033804 // Art2a-ps // ADP-ribosyltransferase 2a, pseudogene // 7 E3|7 54.6 cM // 118	Art2a-ps	0.000107028	-4.18045
NM_001163645 // Osbpl3 // oxysterol binding protein-like 3 // 6|6 B3 // 71720 /// NM_02	Osbpl3	1.62E-06	-4.18628
NM_001205053 // Jdp2 // Jun dimerization protein 2 // 12|12 D3 // 81703 /// NM_030887 /	Jdp2	0.000294276	-4.18732
---		0.00170086	-4.19432
NM_029803 // Ifi27l2a // interferon, alpha-inducible protein 27 like 2A // 12 E|12 // 7	Ifi27l2a	2.47E-05	-4.20999
ENSMUST00000046739 // Ifi44l // interferon-induced protein 44 like // 3 H3|3 76.94 cM /	Ifi44l	0.000295429	-4.21019
NM_181402 // Parp11 // poly (ADP-ribose) polymerase family, member 11 // 6 F3|6 // 1011	Parp11	5.67E-06	-4.23537
NM_009256 // Serpinb9 // serine (or cysteine) peptidase inhibitor, clade B, member 9 //	Serpinb9	2.74E-07	-4.24001
---		1.30E-05	-4.24123
NM_001113379 // Lrrc32 // leucine rich repeat containing 32 // 7 E2|7 53.86 cM // 43421	Lrrc32	1.11E-05	-4.24304
NM_001173460 // Sirpb1b // signal-regulatory protein beta 1B // 3 A1|3 // 668101 /// XM	Sirpb1b	3.01E-06	-4.24787
ENSMUST00000181444 // Gm26589 // predicted gene, 26589 // --- // --- /// XR_379475 // L	Gm26589	6.62E-06	-4.25334
NM_027482 // 5730508B09Rik // RIKEN cDNA 5730508B09 gene // 3|3 H1 // 70617 /// ENSMUST	5730508B09Rik	0.000455534	-4.26705

NM_172689 // Ddx58 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 // 4 A5|4 // 230073 ///	Ddx58	2.81E-05	-4.26729
ENSMUST00000116345 // Gm17193 // predicted gene 17193 // --- // ---	Gm17193	1.12E-05	-4.2831
XM_006535876 // LOC677525 // sp110 nuclear body protein-like // 1|1 // 677525 /// NM_03	LOC677525	6.17E-05	-4.32505
ENSMUST00000032961 // Nupr1 // nuclear protein transcription regulator 1 // 7 F4|7 // 5	Nupr1	1.24E-06	-4.35263
NM_024495 // Car13 // carbonic anhydrase 13 // 3|3 A2 // 71934 /// ENSMUST00000029071 /	Car13	2.69E-05	-4.36196
NM_023141 // Tor3a // torsin family 3, member A // 1 H1|1 // 30935 /// ENSMUST000000796	Tor3a	5.03E-06	-4.38955
NM_001110320 // Cd72 // CD72 antigen // 4 B1|4 23.04 cM // 12517 /// NM_007654 // Cd72	Cd72	1.98E-07	-4.42011
NM_001141948 // Nmi // N-myc (and STAT) interactor // 2|2 C1 // 64685 /// NM_001141949	Nmi	7.63E-06	-4.43269
NM_053108 // Glrx // glutaredoxin // 13 C1|13 40.95 cM // 93692 /// ENSMUST00000022082	Glrx	2.04E-05	-4.43541
NM_001025395 // Src // Rous sarcoma oncogene // 2 H1|2 78.35 cM // 20779 /// NM_009271	Src	3.29E-05	-4.50004
NM_001013817 // Sp140 // Sp140 nuclear body protein // 1 C5|1 // 434484 /// NM_00103790	Sp140	8.98E-06	-4.5092
NM_011930 // Clcn7 // chloride channel 7 // 17 A3.3|17 12.53 cM // 26373 /// ENSMUST000	Clcn7	6.21E-07	-4.52478
---		2.12E-05	-4.52915
NM_213615 // A530032D15Rik // RIKEN cDNA A530032D15Rik gene // 1 C5|1 // 381287 /// ENS	A530032D15Ril	4.54E-06	-4.54266
NM_009767 // Chic1 // cysteine-rich hydrophobic domain 1 // X D|X 42.3 cM // 12212 ///	Chic1	3.51E-06	-4.54985
ENSMUST00000023341 // Cd200 // CD200 antigen // 16 A1|16 29.53 cM // 17470 /// ENSMUST0	Cd200	5.83E-05	-4.55198
NM_145211 // Oas1a // 2-5 oligoadenylate synthetase 1A // 5 F|5 60.65 cM // 246730 ///	Oas1a	3.40E-05	-4.57929
NR_045750 // Gm16675 // predicted gene, 16675 // 8|8 26.42 cM // 100503498 /// ENSMUST0	Gm16675	2.56E-06	-4.64852
NM_008327 // Ifi202b // interferon activated gene 202B // 1 H3|1 // 26388 /// NM_011940	Ifi202b	1.14E-05	-4.66947
NM_001254747 // Il15 // interleukin 15 // 8 C2|8 39.33 cM // 16168 /// NM_008357 // Il1	Il15	0.0001345	-4.68276
NM_001170851 // Klra2 // killer cell lectin-like receptor, subfamily A, member 2 // 6 F	Klra2	7.03E-05	-4.70233
NM_175093 // Trib3 // tribbles homolog 3 (Drosophila) // 2 G3|2 74.83 cM // 228775 ///	Trib3	3.93E-06	-4.70671
NM_001290183 // Ddit3 // DNA-damage inducible transcript 3 // 10 D3|10 // 13198 /// NM_	Ddit3	3.83E-06	-4.71294
ENSMUST00000121995 // Gm15821 // predicted gene 15821 // 17|17 17.98 cM // 100502931 //	Gm15821	3.78E-05	-4.72922
NM_001013817 // Sp140 // Sp140 nuclear body protein // 1 C5|1 // 434484 /// ENSMUST0000	Sp140	0.000788487	-4.74543
NM_001085385 // 1600014C10Rik // RIKEN cDNA 1600014C10 gene // 7|7 B1 // 72244 /// ENSM	1600014C10Rik	4.32E-09	-4.75169
NM_133888 // Smpdl3b // sphingomyelin phosphodiesterase, acid-like 3B // 4 D2.3|4 // 10	Smpdl3b	1.53E-05	-4.76839
ENSMUST00000180685 // Gm26797 // predicted gene, 26797 // --- // ---	Gm26797	0.000154965	-4.78391
---		0.000132551	-4.7846
---		0.000132551	-4.7846
NM_001033207 // Nlrc5 // NLR family, CARD domain containing 5 // 8 C5|8 // 434341 /// X	Nlrc5	0.000329578	-4.78862
NM_001082552 // Trim21 // tripartite motif-containing 21 // 7 F1|7 // 20821 /// NM_0092	Trim21	5.82E-05	-4.80012
ENSMUST00000136366 // Ms4a4b // membrane-spanning 4-domains, subfamily A, member 4B //	Ms4a4b	0.00220551	-4.82228
NM_008479 // Lag3 // lymphocyte-activation gene 3 // 6 F2|6 // 16768 /// ENSMUST0000003	Lag3	2.14E-05	-4.83833
NM_001172205 // Arid5a // AT rich interactive domain 5A (MRF1-like) // 1 B|1 // 214855	Arid5a	2.63E-06	-4.84493
---		1.62E-05	-4.86639
---		1.62E-05	-4.86639
NM_172893 // Parp12 // poly (ADP-ribose) polymerase family, member 12 // 6 B1|6 // 2437	Parp12	1.60E-05	-4.87645
NM_008102 // Gch1 // GTP cyclohydrolase 1 // 14 C2-3|14 24.6 cM // 14528 /// ENSMUST000	Gch1	1.28E-06	-4.89172
NR_045367 // A630012P03Rik // RIKEN cDNA A630012P03 gene // X A5|X // 100504594 /// ENS	A630012P03Rik	6.77E-06	-4.89861
NM_172883 // Mfsd7a // major facilitator superfamily domain containing 7A // 5 F|5 // 2	Mfsd7a	3.02E-06	-4.95515
NM_153511 // Il1f9 // interleukin 1 family, member 9 // 2 A3|2 16.24 cM // 215257 /// E	Il1f9	0.000114605	-4.97272
NM_008655 // Gadd45b // growth arrest and DNA-damage-inducible 45 beta // 10 C1|10 39.7	Gadd45b	1.68E-06	-4.97651
ENSMUST00000173680 // Gm20481 // predicted gene 20481 // --- // --- /// BC054065 // Hsp	Gm20481	1.09E-05	-4.99032
NM_001177752 // Pfkfb3 // 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 // 2 A1	Pfkfb3	7.98E-06	-4.99741
NM_007609 // Casp4 // caspase 4, apoptosis-related cysteine peptidase // 9 A1|9 2.46 cM	Casp4	4.78E-05	-5.02559
NM_019949 // Ube2l6 // ubiquitin-conjugating enzyme E2L 6 // 2|2 E1 // 56791 /// ENSMUS	Ube2l6	2.87E-06	-5.03852
NM_023738 // Uba7 // ubiquitin-like modifier activating enzyme 7 // 9 F2|9 59.07 cM //	Uba7	5.50E-07	-5.05669
XM_006537281 // Psmb9 // proteasome (prosome, macropain) subunit, beta type 9 (large mu	Psmb9	7.32E-07	-5.06058
ENSMUST00000142107 // Gm11626 // predicted gene 11626 // --- // ---	Gm11626	0.000302063	-5.06895
NM_029522 // Gpsm2 // G-protein signalling modulator 2 (AGS3-like, C. elegans) // 3 F3|	Gpsm2	6.59E-07	-5.07121
NM_138953 // Ell2 // elongation factor RNA polymerase II 2 // 13 C1|13 // 192657 /// EN	Ell2	1.58E-06	-5.07632
NM_008311 // Htr2b // 5-hydroxytryptamine (serotonin) receptor 2B // 1 C5|1 // 15559 //	Htr2b	2.26E-06	-5.09236
NM_023456 // Npy // neuropeptide Y // 6 B3|6 24.04 cM // 109648 /// ENSMUST00000031843	Npy	4.11E-05	-5.11978
NR_102296 // C430002N11Rik // RIKEN cDNA C430002N11 gene // 9|9 // 319707 /// NR_102293	C430002N11Ril	0.000451615	-5.1209
ENSMUST00000108349 // LOC100038947 // signal-regulatory protein beta 1-like // 3 A1|3 /	LOC100038947	0.00142378	-5.1267
NM_010531 // Il18bp // interleukin 18 binding protein // 7|7 F1 // 16068 /// ENSMUST000	Il18bp	6.99E-07	-5.12874
NM_007832 // Dck // deoxycytidine kinase // 5 E2|5 // 13178 /// ENSMUST00000031311 // D	Dck	1.08E-06	-5.15303
BC128471 // Unc93a // unc-93 homolog A (C. elegans) // 17 A1|17 8.78 cM // 381058 /// N	Unc93a	0.000402219	-5.15966
NM_008329 // Ifi204 // interferon activated gene 204 // 1 H3|1 80.63 cM // 15951 /// XM	Ifi204	0.000420141	-5.16491
NM_021887 // Il21r // interleukin 21 receptor // 7|7 F4 // 60504 /// XM_006508097 // Il	Il21r	4.38E-08	-5.16695
NM_001004762 // Pla2g4c // phospholipase A2, group IVC (cytosolic, calcium-independent)	Pla2g4c	0.000203398	-5.18152
NM_010398 // H2-T23 // histocompatibility 2, T region locus 23 // 17 B1|17 18.86 cM //	H2-T23	8.46E-07	-5.20484
---		0.00142095	-5.20652
NM_001205313 // Stat1 // signal transducer and activator of transcription 1 // 1 C1.1|1	Stat1	1.04E-05	-5.20773
NM_011817 // Gadd45g // growth arrest and DNA-damage-inducible 45 gamma // 13|13 A5-B /	Gadd45g	2.94E-08	-5.27326
---		0.00020246	-5.2747
XR_378400 // Gm8995 // predicted gene 8995 // 7 E3|7 // 668139 /// ENSMUST00000184842 /	Gm8995	9.65E-06	-5.3384
NR_030719 // Gm8979 // very large inducible GTPase 1 pseudogene // 7 E3|7 // 668108 ///	Gm8979	2.16E-05	-5.35696
NM_001008233 // Plekhn1 // pleckstrin homology domain containing, family N member 1 //	Plekhn1	6.82E-07	-5.38336
XM_006535862 // LOC100041708 // nuclear body protein SP140-like // 1|1 // 100041708	LOC100041708	0.000450999	-5.38792
---		0.000331031	-5.40782
NM_153287 // Csrnp1 // cysteine-serine-rich nuclear protein 1 // 9 F4|9 // 215418 /// X	Csrnp1	5.31E-08	-5.45173
NM_001164477 // Ifih1 // interferon induced with helicase C domain 1 // 2|2 C3 // 71586	Ifih1	0.000399031	-5.45699
NM_001177576 // Slc25a22 // solute carrier family 25 (mitochondrial carrier, glutamate)	Slc25a22	1.16E-07	-5.46451
ENSMUST00000162784 // Gm16094 // predicted gene 16094 // --- // ---	Gm16094	0.000132341	-5.49349
NM_013484 // C2 // complement component 2 (within H-2S) // 17 B1|17 18.41 cM // 12263 /	C2	0.000287264	-5.54593
NR_030719 // Gm8979 // very large inducible GTPase 1 pseudogene // 7 E3|7 // 668108 ///	Gm8979	1.31E-05	-5.56077
NM_008326 // Irgm1 // immunity-related GTPase family M member 1 // 11 B1.2|11 // 15944	Irgm1	2.72E-06	-5.57144
NM_145530 // Rhov // ras homolog gene family, member V // 2 E5|2 // 228543 /// ENSMUST0	Rhov	8.47E-09	-5.57695
NM_001161798 // Mthfr // 5,10-methylenetetrahydrofolate reductase // 4 E2|4 78.67 cM //	Mthfr	2.60E-07	-5.57742
NM_009775 // Tspo // translocator protein // 15 E1|15 39.4 cM // 12257 /// ENSMUST00000	Tspo	6.73E-07	-5.61282
ENSMUST00000103468 // Igh-V11 // immunoglobulin heavy chain (V11 family) // 12 F1|12 //	Igh-V11	0.000175222	-5.61559
---		0.00552939	-5.64947
NM_138682 // Lrrc4 // leucine rich repeat containing 4 // 6 A3.3|6 // 192198 /// ENSMUS	Lrrc4	1.44E-05	-5.65896
AK035387 // Gm20559 // predicted gene, 20559 // 6 A1|6 // 330256	Gm20559	5.36E-07	-5.68786
NM_008380 // Inhba // inhibin beta-A // 13 A1|13 5.85 cM // 16323 /// ENSMUST0000004260	Inhba	6.27E-06	-5.69569
NM_009801 // Car2 // carbonic anhydrase 2 // 3 A1|3 3.23 cM // 12349 /// XM_006530050 /	Car2	0.000945506	-5.765
NM_001033196 // Znfx1 // zinc finger, NFX1-type containing 1 // 2 H3|2 // 98999 /// ENS	Znfx1	1.96E-07	-5.76508

NM_010577 // Itga5 // integrin alpha 5 (fibronectin receptor alpha) // 15 F3|15 58.9 cM	Itga5	2.30E-06	-5.76673
ENSMUST00000172979 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17	H2-Q5	4.88E-05	-5.77922
NM_009742 // Bcl2a1a // B cell leukemia/lymphoma 2 related protein A1a // 9 E3.1|9 47.2	Bcl2a1a	0.000692464	-5.8292
NM_010597 // Kcnab1 // potassium voltage-gated channel, shaker-related subfamily, beta	Kcnab1	2.61E-08	-5.83047
NM_028788 // 1300002K09Rik // RIKEN cDNA 1300002K09 gene // 4 B1|4 // 74152 /// XM_0065	1300002K09Rik	9.55E-08	-5.9135
NM_009630 // Adora2a // adenosine A2a receptor // 10 B5.3|10 // 11540 /// XM_006513094	Adora2a	0.00448167	-5.92243
NM_001033780 // I830077J02Rik // RIKEN cDNA I830077J02 gene // 3 F2.2|3 // 433638 /// X	I830077J02Rik	1.02E-08	-5.93977
NM_010231 // Fmo1 // flavin containing monooxygenase 1 // 1 H1|1 70.34 cM // 14261 ///	Fmo1	3.19E-06	-6.00666
NM_001038643 // Slco3a1 // solute carrier organic anion transporter family, member 3a1	Slco3a1	0.00019235	-6.0429
NM_001161790 // Mefv // Mediterranean fever // 16 A1|16 2.18 cM // 54483 /// NM_0011617	Mefv	0.00126195	-6.04635
NM_007707 // Socs3 // suppressor of cytokine signaling 3 // 11 E2|11 // 12702 /// ENSMU	Socs3	0.00152061	-6.06688
NM_001171007 // Nod1 // nucleotide-binding oligomerization domain containing 1 // 6 B3|	Nod1	7.04E-06	-6.08349
NM_176922 // Itga11 // integrin alpha 11 // 9 B|9 // 319480 /// ENSMUST00000034774 // I	Itga11	1.52E-06	-6.11941
NM_025658 // Ms4a4d // membrane-spanning 4-domains, subfamily A, member 4D // 19 A|19 /	Ms4a4d	6.55E-05	-6.2106
NM_001199733 // Daxx // Fas death domain-associated protein // 17 B1|17 17.98 cM // 131	Daxx	2.70E-05	-6.21615
NM_001198835 // Coch // coagulation factor C homolog (Limulus polyphemus) // 12 C1|12 2	Coch	5.06E-06	-6.2779
NM_001102404 // Acp5 // acid phosphatase 5, tartrate resistant // 9 A3|9 8.38 cM // 114	Acp5	9.37E-07	-6.28295
NM_011141 // Pou3f1 // POU domain, class 3, transcription factor 1 // 4 D2.2|4 57.86 cM	Pou3f1	3.96E-05	-6.36706
XM_006514332 // Misp // mitotic spindle positioning // 10 C1|10 // 78906 /// XM_0065143	Misp	8.99E-06	-6.36845
ENSMUST00000111253 // Setdb2 // SET domain, bifurcated 2 // 14 C3|14 // 239122 /// AK08	Setdb2	2.01E-06	-6.38708
NM_175118 // Dusp28 // dual specificity phosphatase 28 // 1 D|1 // 67446 /// ENSMUST000	Dusp28	6.29E-06	-6.41692
NM_001161730 // Tap1 // transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) //	Tap1	7.14E-06	-6.41798
NM_009776 // Serping1 // serine (or cysteine) peptidase inhibitor, clade G, member 1 //	Serping1	8.83E-06	-6.44144
NM_030150 // Dhx58 // DEXH (Asp-Glu-X-His) box polypeptide 58 // 11 D|11 63.52 cM // 80	Dhx58	5.12E-07	-6.46261
NM_001142952 // Fam46c // family with sequence similarity 46, member C // 3 F2.2|3 // 7	Fam46c	3.72E-07	-6.47253
NM_011852 // Oas1g // 2-5 oligoadenylate synthetase 1G // 5 F|5 60.65 cM // 23960 /// E	Oas1g	1.80E-05	-6.49644
NM_010510 // Ifnb1 // interferon beta 1, fibroblast // 4 C4|4 41.91 cM // 15977 /// ENS	Ifnb1	6.25E-08	-6.51255
NM_172796 // Slfn9 // schlafen 9 // 11 C|11 // 237886 /// ENSMUST00000038211 // Slfn9 /	Slfn9	0.000199195	-6.53247
NM_001045540 // Gm12185 // predicted gene 12185 // 11 B1.2|11 // 620913 /// ENSMUST0000	Gm12185	0.000112523	-6.68304
NM_009156 // Sepw1 // selenoprotein W, muscle 1 // 7|7 A2 // 20364 /// ENSMUST000000443	Sepw1	1.89E-07	-6.80992
NM_008638 // Mthfd2 // methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methen	Mthfd2	2.43E-08	-6.81168
NM_001271603 // Socs1 // suppressor of cytokine signaling 1 // 16 A1|16 5.81 cM // 1270	Socs1	0.00035446	-6.88565
NM_001136082 // Timeless // timeless circadian clock 1 // 10 D3|10 76.49 cM // 21853 //	Timeless	4.68E-07	-6.89628
NM_008247 // Ppap2a // phosphatidic acid phosphatase type 2A // 13 D2.2|13 // 19012 ///	Ppap2a	1.37E-07	-6.89676
ENSMUST00000134150 // Batf2 // basic leucine zipper transcription factor, ATF-like 2 //	Batf2	2.26E-05	-6.94138
NM_001045526 // Scimp // SLP adaptor and CSK interacting membrane protein // 11 B3|11 /	Scimp	5.56E-05	-7.00053
NM_009728 // Atp10a // ATPase, class V, type 10A // 7 C|7 // 11982 /// XM_006540582 //	Atp10a	0.000179495	-7.0125
NM_010397 // H2-T22 // histocompatibility 2, T region locus 22 // 17 B1|17 18.87 cM //	H2-T22	1.97E-06	-7.01566
NM_008013 // Fgl2 // fibrinogen-like protein 2 // 5 A3|5 9.83 cM // 14190 /// ENSMUST00	Fgl2	9.95E-05	-7.02083
NM_001101475 // F830016B08Rik // RIKEN cDNA F830016B08 gene // 18 D3|18 // 240328 /// X	F830016B08Rik	0.0017214	-7.03144
NM_027320 // Ifi35 // interferon-induced protein 35 // 11 D|11 // 70110 /// ENSMUST0000	Ifi35	2.52E-06	-7.04166
NM_011562 // Tdgf1 // teratocarcinoma-derived growth factor 1 // 9 F3|9 60.79 cM // 216	Tdgf1	6.27E-05	-7.07191
NR_040453 // Gm17757 // GTPase, very large interferon inducible 1 pseudogene // 7|7 //	Gm17757	0.000140179	-7.08871
NM_001163440 // Mov10 // Moloney leukemia virus 10 // 3|3 F2 // 17454 /// NM_001163441	Mov10	1.81E-06	-7.11255
NM_001271676 // Ifi47 // interferon gamma inducible protein 47 // 11 B1.2|11 // 15953 /	Ifi47	0.000153421	-7.12242
NM_001163575 // Parp10 // poly (ADP-ribose) polymerase family, member 10 // 15 D3|15 //	Parp10	1.94E-07	-7.13469
NM_019963 // Stat2 // signal transducer and activator of transcription 2 // 10 D3|10 76	Stat2	9.73E-06	-7.16562
NM_029495 // Epsti1 // epithelial stromal interaction 1 (breast) // 14 D3|14 // 108670	Epsti1	7.62E-05	-7.1688
NM_175449 // Fam26f // family with sequence similarity 26, member F // 10 B1|10 // 2159	Fam26f	0.00116948	-7.18224
NM_001252374 // Nt5c3 // 5-nucleotidase, cytosolic III // 6 B3|6 // 107569 /// XM_00650	Nt5c3	2.32E-05	-7.20143
ENSMUST00000144738 // Gm15726 // predicted gene 15726 // --- // ---	Gm15726	2.20E-07	-7.24547
NM_027081 // Dennd6b // DENN/MADD domain containing 6B // 15 E3|15 // 69440 /// ENSMUST	Dennd6b	6.27E-06	-7.2773
NR_040453 // Gm17757 // GTPase, very large interferon inducible 1 pseudogene // 7|7 //	Gm17757	0.000123613	-7.3612
NM_026516 // Tmem178 // transmembrane protein 178 // 17 E3|17 // 68027 /// ENSMUST00000	Tmem178	2.62E-05	-7.44068
NM_001252600 // Irf7 // interferon regulatory factor 7 // 7 F5|7 // 54123 /// NM_001252	Irf7	0.000137396	-7.52212
NM_001290822 // Pdpn // podoplanin // 4 E1|4 // 14726 /// NM_010329 // Pdpn // podoplan	Pdpn	2.67E-09	-7.53565
NM_001243039 // Gm4070 // predicted gene 4070 // 7 E3|7 // 100042856 /// NM_029000 // G	Gm4070	5.83E-05	-7.54067
NM_028270 // Aldh1b1 // aldehyde dehydrogenase 1 family, member B1 // 4|4 B2 // 72535 /	Aldh1b1	1.91E-06	-7.64574
XR_385061 // LOC102632310 // uncharacterized LOC102632310 // --- // 102632310 /// ENSMU	LOC102632310	5.21E-05	-7.67563
NM_022420 // Gprc5b // G protein-coupled receptor, family C, group 5, member B // 7 F3|	Gprc5b	5.28E-07	-7.77616
NM_001033405 // Treml2 // triggering receptor expressed on myeloid cells-like 2 // 17 C	Treml2	3.52E-06	-7.80466
NM_001135115 // Gm12250 // predicted gene 12250 // 11 B1.3|11 // 631323	Gm12250	0.000130021	-7.8447
NM_001243039 // Gm4070 // predicted gene 4070 // 7 E3|7 // 100042856 /// NM_029000 // G	Gm4070	6.88E-06	-7.9238
NM_029005 // Mlkl // mixed lineage kinase domain-like // 8|8 D3 // 74568 /// XM_0065314	Mlkl	6.86E-06	-8.03043
NM_001033339 // Mmp25 // matrix metallopeptidase 25 // 17 A3.3|17 // 240047 /// ENSMUST	Mmp25	0.000261066	-8.12364
NR_033483 // U90926 // cDNA sequence U90926 // 5 E2|5 // 57425 /// ENSMUST00000031356 /	U90926	9.83E-05	-8.17275
NM_001290311 // Wnk2 // WNK lysine deficient protein kinase 2 // 13 B1|13 25.07 cM // 7	Wnk2	8.54E-06	-8.17545
NM_172777 // Gbp9 // guanylate-binding protein 9 // 5 E5|5 // 236573 /// XM_006534923 /	Gbp9	0.000225352	-8.32867
NR_003507 // Oas1b // 2-5 oligoadenylate synthetase 1B // 5 F|5 60.64 cM // 23961 /// E	Oas1b	1.20E-05	-8.33593
NM_172439 // Inpp5j // inositol polyphosphate 5-phosphatase J // 11 A1|11 // 170835 ///	Inpp5j	4.51E-07	-8.4479
NM_019440 // Irgm2 // immunity-related GTPase family M member 2 // 11 B1.3|11 // 54396	Irgm2	2.84E-05	-8.46474
NM_198095 // Bst2 // bone marrow stromal cell antigen 2 // 8 B3.3|8 // 69550 /// ENSMUS	Bst2	1.78E-07	-8.46968
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	3.04E-07	-8.48786
NM_013642 // Dusp1 // dual specificity phosphatase 1 // 17 A2-C|17 13.28 cM // 19252 //	Dusp1	4.32E-10	-8.70016
NR_002687 // Gm5424 // argininosuccinate synthase pseudogene // 10 B4|10 // 432466 ///	Gm5424	6.66E-05	-8.75188
NM_021893 // Cd274 // CD274 antigen // 19|19 C2 // 60533 /// ENSMUST00000016640 // Cd27	Cd274	6.95E-06	-8.78525
NM_172812 // Htr2a // 5-hydroxytryptamine (serotonin) receptor 2A // 14 D2|14 39.37 cM	Htr2a	1.97E-06	-8.7979
NM_001201460 // H2-Q9 // histocompatibility 2, Q region locus 9 // 17|17 // 110558 ///	H2-Q9	2.44E-08	-8.84118
NM_199016 // Enpp4 // ectonucleotide pyrophosphatase/phosphodiesterase 4 // 17 B3|17 //	Enpp4	1.75E-05	-8.95063
NM_001162938 // Pydc3 // pyrin domain containing 3 // 1 H3|1 // 100033459 /// ENSMUST00	Pydc3	0.00116798	-9.06946
NR_030671 // AW011738 // expressed sequence AW011738 // 4 E2|4 // 100382 /// ENSMUST000	AW011738	9.77E-05	-9.07766
NM_025465 // Tma16 // translation machinery associated 16 homolog (S. cerevisiae) // 8|	Tma16	0.000279038	-9.18722
NM_001143689 // H2-Q4 // histocompatibility 2, Q region locus 4 // 17 B1|17 18.65 cM //	H2-Q4	8.96E-07	-9.23657
NM_010751 // Mxd1 // MAX dimerization protein 1 // 6 D1|6 37.75 cM // 17119 /// ENSMUST	Mxd1	8.89E-07	-9.28314
---		5.58E-05	-9.31022
NM_010478 // Hspa1b // heat shock protein 1B // 17 B1|17 18.5 cM // 15511 /// ENSMUST00	Hspa1b	6.26E-05	-9.33951
NM_001037713 // Xaf1 // XIAP associated factor 1 // 11 B4|11 // 327959 /// NM_001291153	Xaf1	1.09E-06	-9.46333
NM_007719 // Ccr7 // chemokine (C-C motif) receptor 7 // 11 D|11 // 12775 /// XM_006532	Ccr7	0.000128619	-9.63209
NM_009421 // Traf1 // TNF receptor-associated factor 1 // 2 B|2 // 22029 /// XM_0064978	Traf1	0.00133631	-9.63789

NM_029509 // Gbp8 // guanylate-binding protein 8 // 5 E5|5 // 76074 /// ENSMUST00000031	Gbp8	2.17E-06	-9.75153
NR_029457 // G530011O06Rik // RIKEN cDNA G530011O06 gene // X and Y|X // 654820 /// ENS	G530011O06Ri	1.85E-07	-9.89493
NM_001083312 // Gbp7 // guanylate binding protein 7 // 3 H1|3 // 229900 /// NM_145545 /	Gbp7	0.00140936	-10.2329
NM_009137 // Ccl22 // chemokine (C-C motif) ligand 22 // 8 C5|8 // 20299 /// ENSMUST000	Ccl22	0.000760111	-10.2535
---		0.000703066	-10.279
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	1.13E-06	-10.414
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	1.13E-06	-10.414
BC096584 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 150	H2-Q5	1.13E-06	-10.414
NM_001293783 // Ddx60 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 // 8 B3.1|8 // 23431	Ddx60	2.19E-05	-10.4395
NM_001039701 // Il1rn // interleukin 1 receptor antagonist // 2 A3|2 16.36 cM // 16181	Il1rn	4.58E-06	-10.7152
NM_009943 // Cox6a2 // cytochrome c oxidase subunit VIa polypeptide 2 // 7 F3|7 70.04 c	Cox6a2	4.16E-07	-10.9401
NM_025992 // Herc6 // hect domain and RLD 6 // 6 C1|6 // 67138 /// ENSMUST00000031817 /	Herc6	7.75E-06	-10.9559
NM_001163014 // Gp6 // glycoprotein 6 (platelet) // 7 A1|7 // 243816 /// XM_006539909 /	Gp6	1.64E-06	-11.0381
NM_030710 // Slamf6 // SLAM family member 6 // 1 H3|1 79.54 cM // 30925 /// XM_00649688	Slamf6	2.92E-08	-11.046
NM_145226 // Oas3 // 2-5 oligoadenylate synthetase 3 // 5 F|5 60.64 cM // 246727 /// EN	Oas3	7.89E-06	-11.1677
NM_001242368 // F10 // coagulation factor X // 8 A1.1|8 5.73 cM // 14058 /// NM_007972	F10	1.22E-05	-11.208
NM_008768 // Orm1 // orosomucoid 1 // 4 B3|4 33.96 cM // 18405 /// ENSMUST00000030044 /	Orm1	0.000386916	-11.2285
NM_017370 // Hp // haptoglobin // 8 D3|8 57.11 cM // 15439 /// ENSMUST00000074898 // Hp	Hp	4.08E-06	-11.5127
ENSMUST00000124513 // Gm15247 // predicted gene 15247 // --- // --- /// AK019053 // Gm1	Gm15247	1.46E-07	-11.6248
NM_021394 // Zbp1 // Z-DNA binding protein 1 // 2 H3|2 // 58203 /// ENSMUST00000029018	Zbp1	2.83E-05	-11.7381
NM_020498 // Ly6i // lymphocyte antigen 6 complex, locus I // 15 D3|15 // 57248 /// ENS	Ly6i	1.26E-06	-11.9537
NM_009369 // Tgfbi // transforming growth factor, beta induced // 13 B-C1|13 30.09 cM /	Tgfbi	4.68E-11	-12.0349
NR_051981 // H2-Q5 // histocompatibility 2, Q region locus 5 // 17 B1|17 19.17 cM // 15	H2-Q5	6.29E-07	-12.1669
NM_183103 // Prss46 // protease, serine 46 // 9 F3|9 60.79 cM // 74306 /// ENSMUST00000	Prss46	6.39E-07	-12.2866
---		0.00203371	-12.6276
NM_001164289 // Phf11c // PHD finger protein 11C // 14 C3|14 // 628705 /// ENSMUST00000	Phf11c	1.25E-05	-12.6431
XR_401026 // A730011C13Rik // RIKEN cDNA A730011C13 gene // 3|3 // 319916 /// ENSMUST00	A730011C13Rik	2.88E-08	-12.6635
---		0.000129178	-12.6988
NM_177363 // Tarm1 // T cell-interacting, activating receptor on myeloid cells 1 // 7 A	Tarm1	0.000234213	-12.8493
ENSMUST00000070435 // Fabp3-ps1 // fatty acid binding protein 3, muscle and heart, pseu	Fabp3-ps1	1.38E-06	-12.8722
ENSMUST00000127563 // Gm13822 // predicted gene 13822 // --- // ---	Gm13822	0.000183986	-13.0386
NM_001271498 // Il15ra // interleukin 15 receptor, alpha chain // 2 A1|2 8.97 cM // 161	Il15ra	6.45E-06	-13.0996
ENSMUST00000057784 // Slc7a2 // solute carrier family 7 (cationic amino acid transporte	Slc7a2	0.000230042	-13.3439
NM_001169153 // Cd300lf // CD300 antigen like family member F // 11 E2|11 // 246746 ///	Cd300lf	3.52E-08	-13.4057
NM_183162 // Helz2 // helicase with zinc finger 2, transcriptional coactivator // 2 H4|	Helz2	2.06E-05	-13.8937
NR_027919 // Bambi-ps1 // BMP and activin membrane-bound inhibitor, pseudogene (Xenopus	Bambi-ps1	4.21E-06	-14.3217
NM_001162883 // Apol9a // apolipoprotein L 9a // 15 E1|15 // 223672 /// NM_173786 // Ap	Apol9a	2.22E-07	-14.3949
NM_013730 // Slamf1 // signaling lymphocytic activation molecule family member 1 // 1 H	Slamf1	0.00320912	-14.4175
NM_021443 // Ccl8 // chemokine (C-C motif) ligand 8 // 11 C|11 49.91 cM // 20307 /// EN	Ccl8	4.28E-06	-14.421
NM_018738 // Igtp // interferon gamma induced GTPase // 11 B1.3|11 36.01 cM // 16145 //	Igtp	4.05E-05	-14.4537
ENSMUST00000103463 // Ighv14-1 // immunoglobulin heavy variable 14-1 // --- // --- ///	Ighv14-1	0.000126507	-14.5173
NM_007981 // Acsl1 // acyl-CoA synthetase long-chain family member 1 // 8|8 B2 // 14081	Acsl1	2.13E-05	-14.8132
ENSMUST00000122664 // n-R5s164 // nuclear encoded rRNA 5S 164 // --- // ---	n-R5s164	5.22E-05	-14.8395
NM_008332 // Ifit2 // interferon-induced protein with tetratricopeptide repeats 2 // 19	Ifit2	0.000556178	-14.9426
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// ENSMUST0000	Gm7609	8.95E-05	-14.9947
NM_001198560 // H2-Q7 // histocompatibility 2, Q region locus 7 // 17 B1|17 18.67 cM //	H2-Q7	1.83E-05	-15.2173
NM_007646 // Cd38 // CD38 antigen // 5 B3|5 23.85 cM // 12494 /// ENSMUST00000030964 //	Cd38	0.00178186	-15.3858
ENSMUST00000031264 // Plac8 // placenta-specific 8 // 5 E3|5 48.49 cM // 231507 /// ENS	Plac8	1.15E-07	-15.4398
ENSMUST00000174699 // H2-Q6 // histocompatibility 2, Q region locus 6 // 17 B1|17 18.66	H2-Q6	5.99E-09	-15.5953
---		0.000302186	-15.6318
XM_006498216 // Ptges // prostaglandin E synthase // 2 B|2 21.75 cM // 64292 /// NM_022	Ptges	0.000139599	-16.0282
NM_199015 // Phf11d // PHD finger protein 11D // 14 C3|14 31.48 cM // 219132 /// XM_006	Phf11d	8.01E-06	-16.2404
NM_001164329 // Gm6904 // predicted gene 6904 // 14 C3|14 // 628693 /// ENSMUST00000168	Gm6904	8.62E-07	-16.6213
NM_015783 // Isg15 // ISG15 ubiquitin-like modifier // 4 E2|4 // 100038882 /// ENSMUST0	Isg15	0.000144816	-16.8385
NM_011331 // Ccl12 // chemokine (C-C motif) ligand 12 // 11 C|11 49.9 cM // 20293 /// E	Ccl12	0.0008682	-16.9561
NR_102366 // AW112010 // expressed sequence AW112010 // 19 A|19 // 107350 /// ENSMUST00	AW112010	0.00174339	-16.9819
NM_001025606 // Tmem171 // transmembrane protein 171 // 13 D1|13 // 380863 /// ENSMUST0	Tmem171	9.08E-07	-17.2789
NM_001164327 // Phf11b // PHD finger protein 11B // 14 C3|14 // 236451 /// ENSMUST00000	Phf11b	2.92E-05	-17.4831
NM_001291220 // Isg20 // interferon-stimulated protein // 7 D3|7 // 57444 /// NM_001113	Isg20	2.91E-05	-17.8265
XR_378392 // Trim30c // tripartite motif-containing 30C // 7 E3|7 // 434219 /// ENSMUST	Trim30c	0.000321372	-18.0485
NM_008491 // Lcn2 // lipocalin 2 // 2 A3|2 22.09 cM // 16819 /// ENSMUST00000050785 //	Lcn2	5.50E-05	-18.1517
XM_006527251 // Ms4a4c // membrane-spanning 4-domains, subfamily A, member 4C // 19 A|1	Ms4a4c	7.55E-05	-18.3302
NM_032541 // Hamp // hepcidin antimicrobial peptide // 7 B1|7 19.27 cM // 84506 /// ENS	Hamp	0.000392925	-18.6505
NM_010260 // Gbp2 // guanylate binding protein 2 // 3 H1|3 66.69 cM // 14469 /// ENSMUS	Gbp2	0.000376301	-18.826
NM_027890 // Susd2 // sushi domain containing 2 // 10|10 B5.3 // 71733 /// ENSMUST00000	Susd2	2.51E-08	-18.8352
---		1.77E-06	-18.8829
XR_397994 // BC023105 // cDNA sequence BC023105 // 18 D3|18 // 667597 /// ENSMUST000000	BC023105	1.01E-05	-19.4826
NM_001013832 // Gpr31b // G protein-coupled receptor 31, D17Leh66b region // 17 A1|17 8	Gpr31b	2.58E-05	-19.7847
NM_010479 // Hspa1a // heat shock protein 1A // 17 B1|17 18.51 cM // 193740 /// ENSMUST	Hspa1a	1.63E-06	-20.2312
NM_001164059 // Sell // selectin, lymphocyte // 1 H2.2|1 71.37 cM // 20343 /// NM_01134	Sell	3.50E-08	-20.3183
NM_172621 // Clic5 // chloride intracellular channel 5 // 17|17 C // 224796 /// XM_0065	Clic5	2.60E-06	-20.6164
NM_011909 // Usp18 // ubiquitin specific peptidase 18 // 6 F|6 57.17 cM // 24110 /// EN	Usp18	1.49E-05	-21.2011
NM_008392 // Irg1 // immunoresponsive gene 1 // 14 E2.3|14 51.67 cM // 16365 /// XM_006	Irg1	0.0042112	-21.4099
NM_001099217 // Ly6c2 // lymphocyte antigen 6 complex, locus C2 // 15 D3|15 // 10004154	Ly6c2	2.15E-07	-21.6159
NR_027852 // Cd40 // CD40 antigen // 2 H3|2 85.38 cM // 21939 /// ENSMUST00000017799 //	Cd40	0.00375845	-21.756
NM_144548 // Il23r // interleukin 23 receptor // 6 C1|6 // 209590 /// ENSMUST0000011836	Il23r	1.46E-06	-22.1005
NM_009425 // Tnfsf10 // tumor necrosis factor (ligand) superfamily, member 10 // 3 A3|3	Tnfsf10	0.00107093	-22.3176
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	1.32E-06	-22.7148
NM_001037925 // BC147527 // cDNA sequence BC147527 // 13|13 // 625360 /// XM_006517732	BC147527	2.86E-06	-22.8038
NM_029612 // Slamf9 // SLAM family member 9 // 1 H3|1 // 98365 /// XM_006497067 // Slam	Slamf9	1.18E-06	-23.4245
NM_001198560 // H2-Q7 // histocompatibility 2, Q region locus 7 // 17 B1|17 18.67 cM //	H2-Q7	2.04E-08	-23.8557
ENSMUST00000093501 // A530040E14Rik // RIKEN cDNA A530040E14 gene // 1 C5|1 // 621875 /	A530040E14Rik	0.00030879	-24.2122
NM_001045543 // Heatr9 // HEAT repeat containing 9 // 11 C|11 // 629303 // XM_00653390	Heatr9	2.44E-06	-24.4061
NM_001177471 // Gm15056 // predicted gene 15056 // 8 A2|8 // 100504014 /// ENSMUST00000	Gm15056	5.18E-06	-24.7977
NM_008331 // Ifit1 // interferon-induced protein with tetratricopeptide repeats 1 // 19	Ifit1	0.000411406	-26.1016
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	1.28E-07	-27.0713
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	3.90E-07	-27.755
NM_001081746 // Gm7609 // predicted pseudogene 7609 // 1 C5|1 // 665378 /// NM_033616 /	Gm7609	3.90E-07	-27.755
NM_001168660 // Apol9b // apolipoprotein L 9b // 15 E1|15 // 71898 /// NM_173743 // Apo	Apol9b	8.37E-06	-27.8129

NM_001033767 // Gm4951 // predicted gene 4951 // 18 D3|18 // 240327 /// ENSMUST00000031	Gm4951	0.000191468	-28.0123
NR_029565 // Mir155 // microRNA 155 // 16|16 // 387173 /// ENSMUST00000083463 // Mir155	Mir155	0.00403794	-28.4615
NM_010612 // Kdr // kinase insert domain protein receptor // 5 C3.3|5 40.23 cM // 16542	Kdr	6.78E-07	-28.6334
NM_001289492 // Gbp3 // guanylate binding protein 3 // 3 H1|3 // 55932 /// NM_001289493	Gbp3	0.000701966	-29.3378
NM_013606 // Mx2 // myxovirus (influenza virus) resistance 2 // 16 C4|16 57.51 cM // 17	Mx2	5.77E-05	-31.2033
NM_175026 // Pyhin1 // pyrin and HIN domain family, member 1 // 1 H3|1 // 236312 /// EN	Pyhin1	8.94E-05	-31.2319
NM_020557 // Cmpk2 // cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial // 12 A2	Cmpk2	0.000456953	-31.3415
NM_153564 // Gbp5 // guanylate binding protein 5 // 3 H1|3 // 229898 /// ENSMUST0000009	Gbp5	0.00366419	-31.4906
NM_008204 // H2-M2 // histocompatibility 2, M region locus 2 // 17 B1|17 19.16 cM // 14	H2-M2	9.61E-06	6.23E-07
NM_001083322 // Klrk1 // killer cell lectin-like receptor subfamily K, member 1 // 6 F3	Klrk1	3.02E-05	-34.5985
NM_001177349 // Pydc4 // pyrin domain containing 4 // 1 H3|1 // 623121 /// NM_001177350	Pydc4	9.90E-07	-34.7497
NM_172603 // Phf11a // PHD finger protein 11A // 14 C3|14 // 219131 /// ENSMUST00000062	Phf11a	4.86E-05	-36.4006
NM_001271416 // Ly6a // lymphocyte antigen 6 complex, locus A // 15 D3|15 34.29 cM // 1	Ly6a	6.05E-10	-37.3877
NM_145209 // Oasl1 // 2-5 oligoadenylate synthetase-like 1 // 5 F|5 // 231655 /// ENSMU	Oasl1	6.01E-05	-38.3046
NM_011246 // Rasgrp1 // RAS guanyl releasing protein 1 // 2 E5|2 59.19 cM // 19419 ///	Rasgrp1	0.00022037	-40.075
NM_010846 // Mx1 // myxovirus (influenza virus) resistance 1 // 16 C4|16 57.46 cM // 17	Mx1	0.000196796	-40.6093
NM_001256005 // Gbp4 // guanylate binding protein 4 // 5 E5|5 50.68 cM // 17472 /// ENS	Gbp4	0.000214556	-43.9247
ENSMUST00000090406 // BC094916 // cDNA sequence BC094916 // 1 H3|1 // 545384 /// ENSMUS	BC094916	4.77E-05	-52.3816
NM_001146275 // Iigp1 // interferon inducible GTPase 1 // 18 D3|18 // 60440 /// ENSMUST	Iigp1	0.000263071	-52.5602
ENSMUST00000137792 // Rsad2 // radical S-adenosyl methionine domain containing 2 // 12|	Rsad2	0.000113028	-53.0382
ENSMUST00000047498 // AA467197 // expressed sequence AA467197 // 2 E5|2 // 433470 /// N	AA467197	8.30E-05	-56.8339
NM_001039646 // Gbp10 // guanylate-binding protein 10 // 5 E5|5 // 626578 /// ENSMUST00	Gbp10	6.99E-05	-58.3462
ENSMUST00000128411 // Tgtp2 // T cell specific GTPase 2 // 11 B1.2|11 // 100039796 ///	Tgtp2	0.000266187	-71.187
NM_172648 // Ifi205 // interferon activated gene 205 // 1 H3|1 80.83 cM // 226695 /// E	Ifi205	0.00109062	-71.4535
XM_003945749 // LOC630751 // interferon-inducible GTPase 1-like // --- // 630751 /// XR	LOC630751	3.92E-05	-77.0482
NM_001167828 // Trim30d // tripartite motif-containing 30D // 7 E3|7 // 209387 /// NM_1	Trim30d	0.000185465	-80.507
NM_008599 // Cxcl9 // chemokine (C-X-C motif) ligand 9 // 5 E2|5 46.51 cM // 17329 ///	Cxcl9	0.000569276	-83.4258
NM_001110517 // Gm14446 // predicted gene 14446 // 19 C1|19 // 667373	Gm14446	3.38E-07	-83.8296
NM_021274 // Cxcl10 // chemokine (C-X-C motif) ligand 10 // 5 E2|5 46.57 cM // 15945 //	Cxcl10	0.00116546	-96.7691
NM_001142706 // Cfb // complement factor B // 17 B1|17 18.41 cM // 14962 /// NM_008198	Cfb	0.000452834	-103.398
NM_009977 // Cst7 // cystatin F (leukocystatin) // 2|2 G1-G3 // 13011 /// ENSMUST000000	Cst7	9.03E-06	-110.042
NM_001039647 // Gbp11 // guanylate binding protein 11 // 5 E5|5 // 634650 /// ENSMUST00	Gbp11	4.41E-05	-112.616
NM_010927 // Nos2 // nitric oxide synthase 2, inducible // 11 B5|11 46.74 cM // 18126 /	Nos2	0.000344268	-169.378
NM_011410 // Slfn4 // schlafen 4 // 11 C|11 // 20558 /// ENSMUST00000000208 // Slfn4 //	Slfn4	9.12E-05	-187.205
NM_011407 // Slfn1 // schlafen 1 // 11 C|11 50.3 cM // 20555 /// ENSMUST00000037994 //	Slfn1	2.39E-05	-237.965
NM_019494 // Cxcl11 // chemokine (C-X-C motif) ligand 11 // 5|5 E3 // 56066 /// NR_0381	Cxcl11	0.00134012	-258.558

Online Repository Results

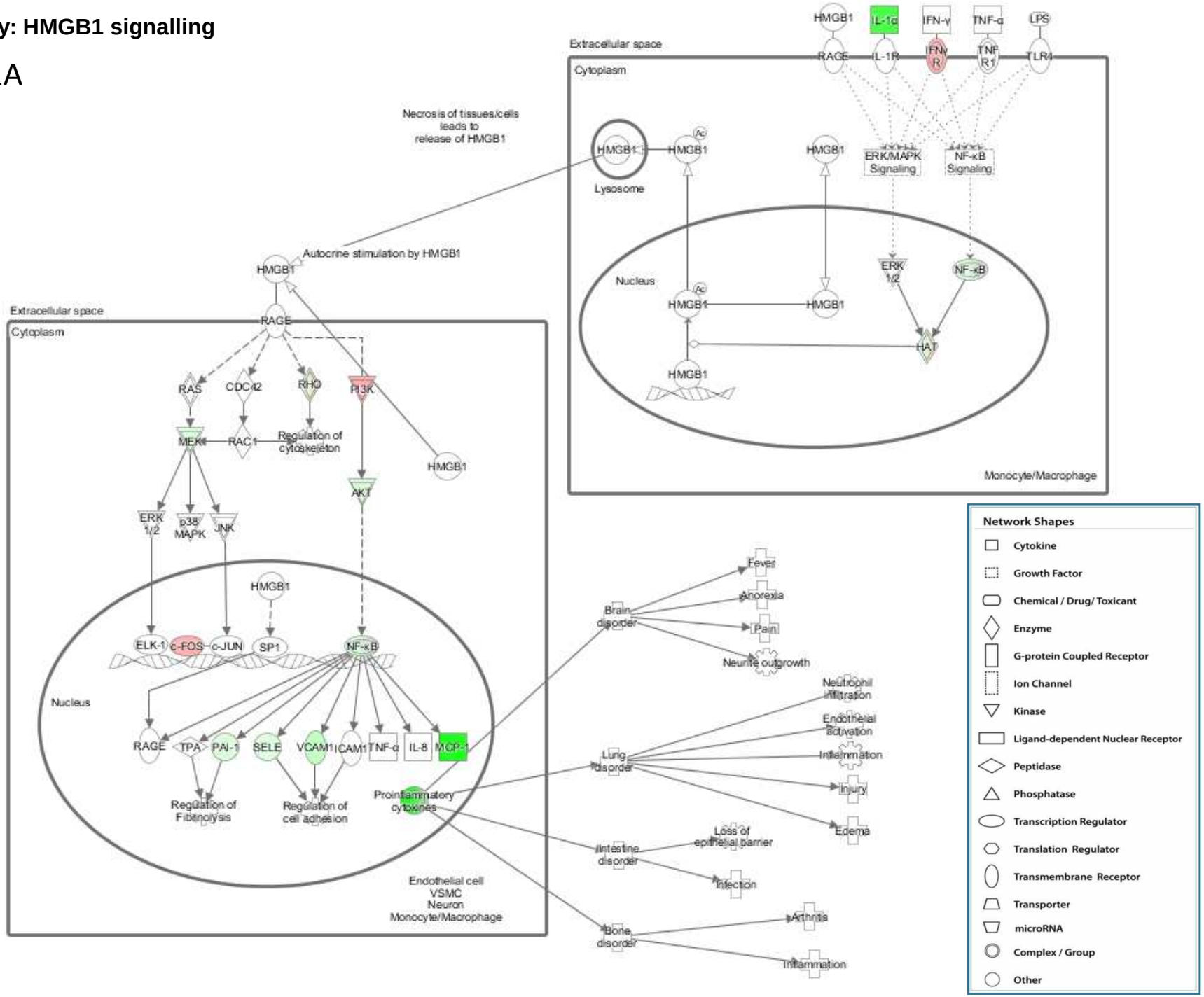
Table 2: Chemokine and cytokine expression in BALF

Cytokine/Chemokine	Vehicle (PBS)	House dust mite	House dust mite + FhHDM-1	*P*
IL-25/IL-17E	ND	ND	ND	
IL-23	ND	ND	ND	
IL-33	ND	ND	ND	
IFN-γ	ND	ND	ND	
IL-1β	ND	ND	ND	
IL-12p40	ND	ND	ND	
IL-12p70	ND	ND	ND	
IL-15	ND	ND	ND	
IL-13	ND	ND	ND	
RANTES	0.39 ± 0.09	0.84 ± 0.23	0.63 ± 0.16	NS
IL-9	50.94 ± 7.05	24.64 ± 4.10	24.29 ± 4.66	NS
Eotaxin	4.92 ± 1.03	15.29 ± 2.97	13.78 ± 4.81	NS
IL-17	0.07 ± 0.06	29.64 ± 13.11	5.62 ± 2.39	NS
IL-4	0.21 ± 0.08	15.64 ± 3.52	8.91 ± 3.28	NS
IL-22	0.65 ± 0.09	4.43 ± 0.78	2.31 ± 0.44	*
GM-CSF	0.29 ± 0.12	2.69 ± 0.93	0.50 ± 0.47	*
IL-6	0.16 ± 0.09	74.20 ± 21.45	20.69 ± 7.53	*
CCL2 (MCP-1)	0	4.79 ± 2.11	0	*
TNF	0.13 ± 0.04	2.94 ± 0.7	0.90 ± 0.30	**
IL-5	1.57 ± 0.29	61.81 ± 17.83	11.10 ± 3.12	**
CXCL1 (KC)	12.05 ± 1.51	120.71 ± 17.63	49.19 ± 11.61	***

Data represent mean (pg/ml) ± SEM. **P* < .05, ***P* < .01, ****P* < .001 in house dust mite vs house dust mite + FhHDM-1 groups. N = 12 mice per group. ND, not detectable; NS, not significant.

IPA Pathway: HMGB1 signalling

Figure E1A



IPA Pathway: The role of IL-17 in the allergic inflammatory airway pathway

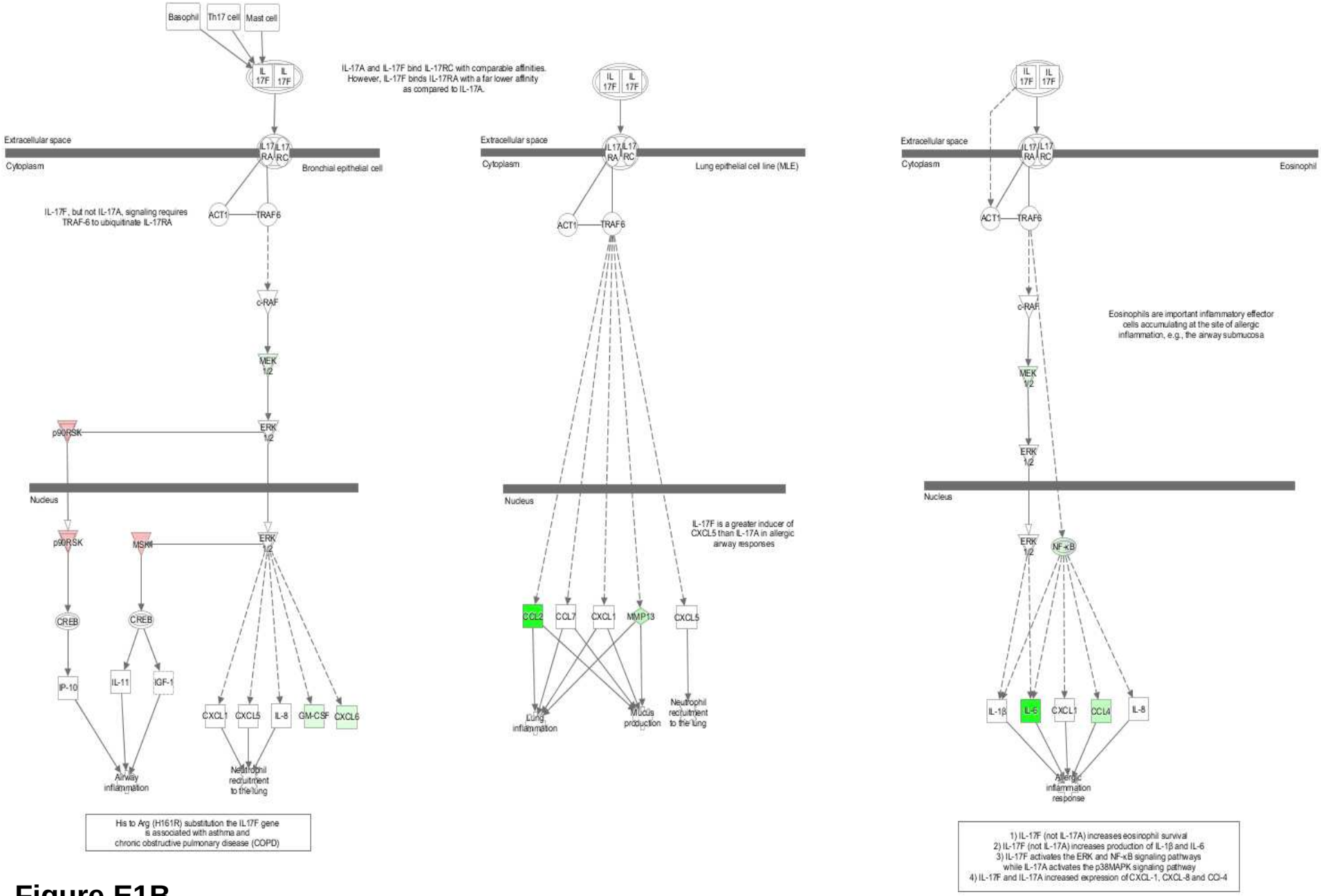


Figure E1B

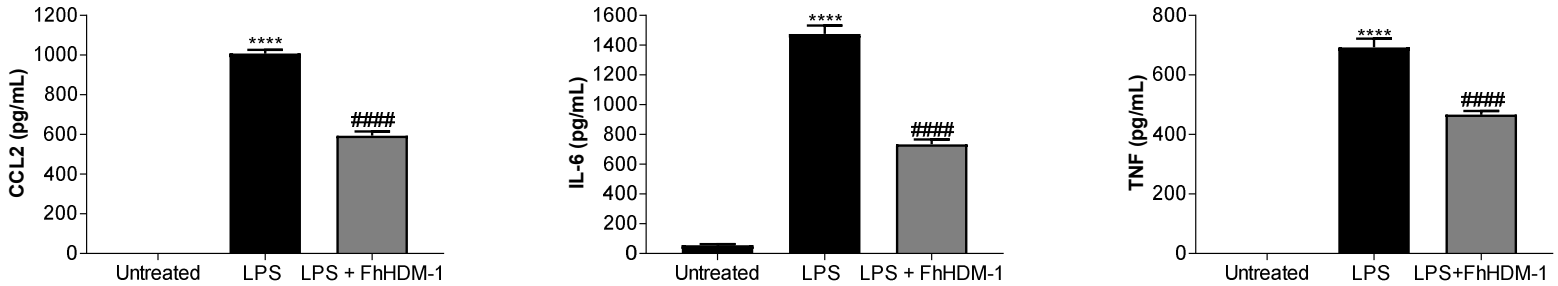
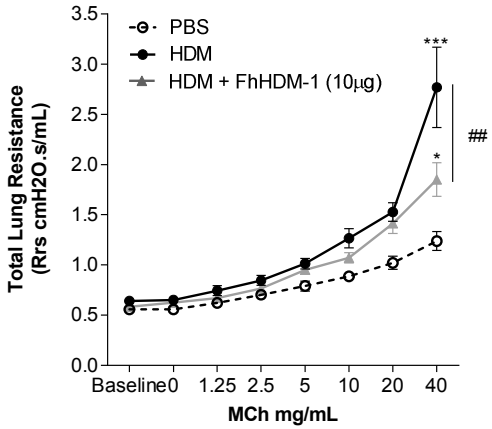

CCL2 (pg/mL)
1200
1000
800
600
400
200
0
****
####
Untreated
LPS
LPS + FhHDM-1
IL-6 (pg/mL)
1600
1400
1200
1000
800
600
400
200
0
****
####
Untreated
LPS
LPS + FhHDM-1
TNF (pg/mL)
800
600
400
200
0
****
####
Untreated
LPS
LPS+FhHDM-1

Fig E2


PBS
HDM
HDM + FhHDM-1 (10μg)
Total Lung Resistance (Rrs cmH2O.s/mL)
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
***
*
##
Baseline0 1.25 2.5 5 10 20 40
MCh mg/mL

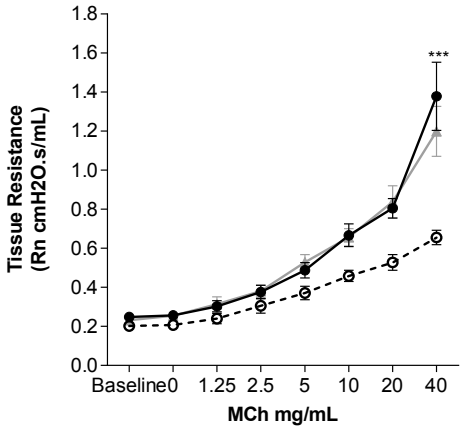

Tissue Resistance (Rn cmH2O.s/mL)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
***
Baseline0 1.25 2.5 5 10 20 40
MCh mg/mL

Fig E3

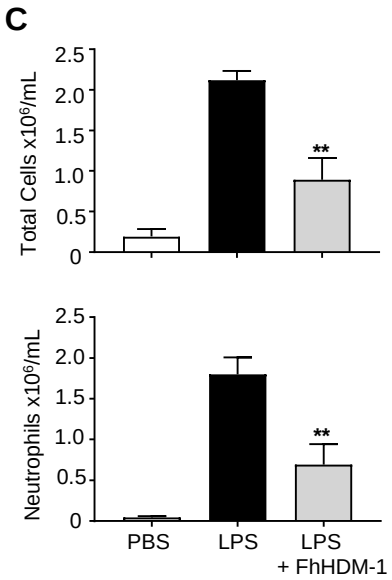

C
Total Cells x10⁶/mL
2.5
2.0
1.5
1.0
0.5
0
**
Neutrophils x10⁶/mL
2.5
2.0
1.5
1.0
0.5
0
**
PBS
LPS
LPS
+ FhHDM-1

Fig E4